	1	11	21	31	41	51	61	71	81	91
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					*********	***********				
SEQ 3			MTVAD	IDVPPAEGIP	YFTPAQNPPA	GTAANPOTN-	GOKIPKLF	TPLTIR-GVT	FQ	NRLGLAPLCQ
SEQ 6			MSQPVVPD	IENKPAPGIS PAVTKSSSTP	VYTDANNICGA	ALHDDDDDT.	SAPPELF	PDIATE-MAT	I.Kananana	NRIGISPICO NRIGISPICO
SEQ 8 SEQ 10				VENTPAAGIP						
SEQ 12			MIVPYOVKPS	DEIKGAPEVS	YYTPEOPVPA	GTFYPOSSD-	EVAPKIF	OPLKIG-KLA	LP	NRIGVSPMCO
SEO 14						MENN	NTIPALF	QPIKISDSIT	LP	NRIGVSPMCM
SEQ 16			MADFTOKK	TSSPAAPGVP	FYTPAQVPAA	GTPLPSTPG-	DVPTLP	TPLKIR-GVE	LQ	NRFAVAPMCT
SEQ 19										
SEQ 22			MSAEKK	TLSKPAAGVP	YYTPAQEPPA	GTPLQQQDA-	IPTLP	KPLKIR-GVE	LS	NRFGVSPMCT
SEQ 24				IVNEGAENVG TANKAAPGVP						
SEQ 27				IDNVAAEGVP						
SEQ 30 SEO 33			MAIDI	IDNVAREGVE	IIIPAQDEFA	GIVISG	31KDF	IFITIR-GVI		MEDITALICO
SEO 35				IINKEAPNVP						
SEQ 38			ARGI	IDNIAAEGAP	YYTPAQD.PA	GTOTSGST	KVF	T.ITIR-GVT	PP	NRLFLAPLCO
SEQ 40								LKIR-GLT	10	NRIMLRGLCQ
SEQ 42										
SEQ 44										
SEQ 83	MTVQSQQQSQ	AI PVLSSQNG	TEPODANKEV	VQNVAAKGVQ	YFNPEQLPAP	GLGINGPNNT	LPKVF	TPIKIR-GMT	MP	NRIWVSPMCQ
SEQ 85		MDTS	REVSGLTPPL	VD\$IDALKIS	NEVPTRSGHP	PPGSVPESIL	PEGVKKPALP	QTLTLP-PAA	PEQAGRMIFK	NRIIVSPMCQ
Bacteria T44612							MSALP	EPYTLK - DVT	I.R	NRIAIPPMCO
NP 625402										
NP 295913										
AF320254				RLRDAGWLEG						
OYE family	<b>-</b> -									
Af4875						MREEPSSAQ-	LF	KPLKVGRC	HLQ	HRMIMAPTTR
A£4961					МТІ	RKLDGEESM-	LP	QPLEIA-NGR	IRLS	HRVVHAPMTR
Ca2460				MTVESTNS						
Nc4452 ScOYE1				MS						
ScOYE2				МР						
ScOYE3				MP						
A36990				MTIESTNS	<b>FVVPSDTKLI</b>	DVTPLGSTK-	LF	QPIKVG-NNV	LP	QRIAYVPTTR
	101	111	121	131	141	151	161	171	181	191
	2		3			4				-5
aro a	2		3	•		4				-5
SEQ 3	2 **	QDGHM	TDYHIAHL	GGIAORGPGL	MLIEATAVQP	E-GRITPQDV	GLWKDS	QIAPMR	RVI-DFVHSQ	GQ-KIGVQ
SEQ 6	2 YSA YSA	QDGHM	TDYHIAHL TPWHMAHL	GGIAQRGPGL GGIAQRGPGP	MLI EATAVOP LMVEATAVEP	E-GRITPQDV B-GRITPQDL	GLWKDS	QIAPMR	RVI-DFVHSQ RVI-EFVHSQ	GQ-KIGV-Q
	2	QDGHM DDGHM DPSSPHVGAL	TDYHIAHL TPWHMAHL TNYHLAHL	GGIAORGPGL GGIAORGPGP GHLALKGAGL	MLIEATAVOP LMVEATAVEP VFIEATAVOP	E-GRITPQDV E-GRITPQDL N-GRISPNDS	GLWKDS GLWKDS GLWQDG	QIAPMRQIEPLS TTSEQFLGLK	RVI-DFVHSQ RVI-EFVHSQ RVV-EFMHAQ	GQ-KIGV-Q NQ-LIGV-Q GA-KVGI-Q
SEQ 6 SEQ 8	YSA	QDGHMDDGHM DPSSPHVGALEDGHM	TD-YHIAHL TP-WHMAHL TN-YHLAHL TD-YHIAHL TP-YHLIHY	GGIAQRGPGL GGIAQRGPGP GHLALKGAGL GGIAQRGPGL GSLVNRGPGI	MLIEATAVOP LMVEATAVEP VFIEATAVOP MMIEATSVSP TIVESTAVSP	E-GRITPQDV B-GRITPQDL N-GRISPNDS B-GRITPQDV E-GGLSPHDL	GLWKDS GLWKDS GLWQDG GLWKDS GIWKDE	QIAPMRQIEPLS TTSEQFLGLKQIAPMK	RVI-DFVHSQ RVI-EFVHSQ RVV-EFMHAQ RVI-DFVHSQ PIV-DYAHSQ	GQ-KIGVQ NQ-LIGVQ GA-KVGIQ SQ-KIGVQ KQ-LIAIQ
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14	YSA	QDGHMDDGHM DPSSPHVGALEDGHM	TDYHIAHL TPWHMAHL TDYHLAHL TDYHIAHL TPYHLIHY TLFHFVHY	GGIAORGPGL GGIAORGPGP GHLALKGAGL GGIAORGPGL GSLVNRGPGI GSFAVRGPAL	MLIEATAVOP IMVEATAVEP VFIEATAVOP MMIEATSVSP TIVESTAVSP IILESIFVSE	E-GRITPQDV B-GRITPQDL N-GRISPNDS B-GRITPQDV B-GGLSPHDL N-SGLSIHDL	GLWKDS GLWKDS GLWCDG GLWKDS GIWKDE GLWNDD	QIAPMRQIEPLS TTSEQFLGLKQIAPMKQAPKLKQAHSLR	RVI-DPVHSQ RVI-EPVHSQ RVI-EPWHAQ RVI-DPVHSQ PIV-DYAHSQ FIV-DPIHDQ	-5
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16	YSA	QDGHMDDGHM DPSSPHVGALEDGHMDYNFEASPTDNQA	TDYHIAHL TPWHMAHL TDYHIAHL TDYHIAHL TDYHLIHY TLFHFVHY TDWHLVHL	GGIAQRGPGL GGIAQRGPGP GHLALKGAGL GGIAQRGPGL GSLVNRGPGI GSFAVRGPAL GSFALRGVPL	MLIEATAVOP LMVEATAVEP VFIEATAVOP MMIEATSVSP TIVESTAVSP TILESIFVSE TIPEATGVLP	E-GRITPQDV B-GRITPQDL N-GRISPNDS B-GRITPQDV E-GGLSPHDL N-SGLSIHDL N-SGLSIHDL	GLWKDSGLWQDGGLWKDSGLWKDSGLWKDSGLWKDBGLWQDS	QIAPMRQIEPLS TTSEQFLGLKQAEKLKQAEKLKQAHSLR	RVI-DFVHSQ RVI-EFVHSQ RVI-EFWHSQ RVI-DFVHSQ PIV-DYAHSQ KIV-DFIHDQ RIV-DYIHSQ	-5
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19	YSA	QDGHMDDGHM DPSSPHVGALEDGHM	TDYHIAHL TPWHMAHL TDYHIAHL TDYHIHY TLFHPVHY TDWHLVHL PNPELAAV	* GGIAORGPGL GGIAORGPGP GHLALKGAGL GGIAORGPGL GSLVNRGPGI GSFAVRGPAL GSFALRGVPL YATWARGDMG	MLIEATAVQP LMVEATAVEP VPIEATAVQP MMIEATSVSP TIVESTAVSP IILESIFVSE TIPEATGVLP LILTGNVQVD	E-GRITPQDV B-GRITPQDV N-GRISPNDS B-GRITPQDV E-GGLSPHDL N-SGLSIHDL N-GRITPECS HAHKGDAHDI	GLWKDSGLWKDSGLWQDGGLWKDSGLWNDEGLWODSGLWODS	QIAPMRQIEPLS TTSEQFLGLKQIAPMKQAEKLKQAHSLRQIAPLK TTPEQTVTAF	RVI-DPVHSQ RVI-EPVHSQ RVV-EPMHAQ RVI-DFVHSQ PIV-DPIHDQ KIV-DPIHDQ RIV-DYIHSQ KAWADAARLN	GO-KIGV-Q NO-LIGV-Q GA-KVGI-Q SQ-KIGV-O KQ-LIAI-Q DG-ICCI-Q GQ-KAGI-Q GOSKTFVVVQ
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22	2	QDGHMDDGHM DPSSPHVGALDYNFEASPTDNQADDGHM	TDYHIAHL TDYHIAHL TDYHIAHL TDYHIAHL TCWHIAHL TCWHICHL TCWHICHL PNPELAAV TDFHLVHL	* GGIAORGPGL GGIAORGPGF GHLALKGAGL GGIAORGPGG GSLVNRGPGI GSFAVRGPAL GSFALRGVPL YATWARGDWG GOFALHGTAL	MLIEATAVQP LMVEATAVEP VPIEATAVQP MMIEATSVSP TIVESTAVSP IILESIFVSE TIPEATGVLP LILTGNVQVD TIVEATSVTP	E-GRITPQDV E-GRITPQDV N-GRISPNDS E-GRITPQDV N-SGLSPHDL N-SGLSIHDL N-GRITPECS N-GRITPECS N-GRITPECS	GLWKDSGLWCDGGLWCDGGLWKDEGLWNDDGLWODSSPNHPGGLWODS		RVI-DFVHSQ RVI-EFVHSQ RVV-EFMHAQ RVI-DFVHSQ FIV-DYAHSQ KIV-DFIHDQ RIV-DYIHSQ KAWADAARLM RIV-DYVHSQ	-5 NQ-LIGV-Q NQ-LIGV-Q GA-KVGI-Q SQ-KIGV-O KQ-LIAI-Q DG-ICCI-Q GQ-KAGI-Q GQ-KTPVVVQ GQ-KTAI-Q
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24	YSA	QDGHMDDGHM DPSSPHVGAL	TDYHIAHL TPYHIAHL TDYHIAHL TPYHIHH TLFHFVHY TDWHLVHL PNPELAAV TDFHLVHL TDFHLVHL TDFHLVHL	*GGIAORGPGL GGIAORGPGP GHLALKGAGL GGIAORGPGL GSLVNRGPGI GSFAVRGPAL GSFALRGVPL YATWARGDWG GOFALHGTAL GAMGMRGPGL	MLIEATAVQP LMVEATAVEP VFIEATAVQP MMIEATSVSP TIVESTAVSP TILESIFVSE TIPEATGVLP LILTGNVQVD TIVEATSVTP VMVEATAVSP	E-GRITPQDV B-GRITPQDV N-GRISPNDS E-GRITPQDV N-SGLSIHDL N-GRITPECS HAHKGDAHDI N-GRISPEDS E-GRISPNDS	GLWKDSGLWCDGGLWCDGGLWCDGGLWCDGGLWCDGGLWQDSSPNHPGGLWQDSGLWGDS	QIAPMRQIEPLS TTSEQFLGLK	RVI-DFVHSQ RVI-EFVHSQ RVV-EFMHAQ RVI-DFVHSQ FIV-DYAHSQ KIV-DFIHDQ RIV-DYIHSQ KAWADAARLIN RIV-DYVHSQ RIV-EFAHSQ	GO-KIGVQ NQ-LIGVQ GA-KVGIQ SQ-KIGVQ KO-LIAIQ DG-ICCIQ GG-KAGIQ GO-KAGIQ GO-KIAIQ NQ-KIGIQ
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22	2	QDGHMDDGHM DPSSPHVGALDYNFEASPTDNQADQGHMFGNHL	TDYHIAHL TPWHMAHL TDYHIAHL TDYHIAHL TPYHLIHY TLFHFVHY TDWHLVHL TDFHLVHL TDFHLVHL TDFHLVHL TDFHLVHL	* GGIAORGPGL GGIAORGPGF GHLALKGAGL GGIAORGPGG GSLVNRGPGI GSFAVRGPAL GSFALRGVPL YATWARGDWG GOFALHGTAL	MLI EATAVQP LMVEATAVEP VPI EATAVQP MMI EATSVSP TIVESTAVSP IILES I FVSE TIPEATGVLP LILTGNVQVD TIVEATSVTP VMVEATAVSP SMVEATAVEA	E-GRITPQDV E-GRITPQDL N-GRISPNDS E-GRITPQDV N-GRITPECS HAHKGDAHDI N-GRISPEDS E-GRISPNDS R-GRISPEDV	GLWKDSGLWKDSGLWCDGGLWKDBGLWNDBGLWODSSPNHPGGLWODSGLWODS	QIAPMRQIEPLS TTSEQFIGLK	RVI-DPVHSQ RVI-EPVHSQ RVI-EPWHAQ RVI-DPVHSQ PIV-DYAHSQ KIV-DPIHDQ RIV-DYIHSQ KAWADARLN RIV-DYVHSQ RIV-EFAHSQ RIV-EFAHSQ RIV-DFIHSQ	-5
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 31	2		TDYHIAHL TPWHMAHL TNYHIAHL TDYHIAHL TPYHLHY TLFHFVHY TDWHLYHL PNPELAAV TDFHLVHL TDFHLVHL TDYHLVHL TDWHLTHL TDWHLTHL	GGIAQRGPGL GGIAQRGPGP GHLALKGAGL GGIAQRGPGL GSLAVRGPGI GSFAVRGPAL YATHARGDWG GQFALHGTAL GAMGMRGPGL GQFALHGAAL GGIIQRGPGL	MLI EATAVOP LMVEATAVEP VFIEATAVOP MMI EATSVSP TIVESTAVSP TIVESTAVSP TIFEATGVLP LILIGATOVOP TIVEATSVTP VMVEATAVSP SMVEATAVON	E-GRITPODV B-GRITPODL N-GRISPNDS B-GRISPNDS H-GGLS+HDL N-GRISPEDS HAHRIDAHDI N-GRISPEDS R-GRISPEDS R-GRISPEDV H-GRITPODV	GLMK - DS GLMC - DS	OIAPMR OIEPLS TTSEOFIGLK OIAPMK OAEKLK OAKLK OIAPLK TTPEOTVTAF OIAPLK TTPEOTVTAF OIAPLK OMPLR OHPLK OIAPLK	RVI-DPVHSQ RVI-EPVHSQ RVI-EPVHSQ PVI-DPVHSQ PIV-DYAHSQ KIV-DPIHDQ KAWADARLM RIV-DVVHSQ RIV-DPVHSQ RIV-DFHSQ RIV-DFHSQ RIV-TFAHSQ	-5
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 31 SEQ 31 SEQ 35	2		TD-YHIAHL TP-WHMAHL TP-YHAHL TD-YHIAHL TD-YHIAHL TP-YHLHY TD-WHLWHL TD-FHVYH TD-FHLVHL TD-FHLVHL TD-HLVHL TD-WHLTHL TD-WHLTHL TD-WHLTHL	GGIAORGPGL GGIAORGPGL GGIAORGPGL GHLALKGAGL GGIAORGPGL GSFAVRGPAL GSFALRGVPL YATWARGDWG GOFALHGTAL GOFALHGTAL GOFALHGAAL GGIIORGPGL	MLIEATAVQP LMVEATAVEP VFIEATAVQP MIEATSVSP TIVESTAVSP TILESIFVSE TIFEATGVLP LILTGNVQVD LILTGNVQVD TIVEATAVEA SMVEATAVEA SMVEATAVEA SMVEATAVQN	E-GRITPODV B-GRITPODV B-GRITPODV B-GRITPODV B-GRISPHDL N-GRISTHDL N-GRISTHDL N-GRITPECS HAHKGDAHDI N-GRISPEDS B-GRISPHDS B-GRISPHDS H-GRISPHDV H-GRITPODV		OLAPMR	RVI-DPVHSQ RVI-EPVHSQ RVI-EPVHSQ RVI-DPVHSQ FIV-DYHHSQ RIV-DYTHSQ KAWADAARLM RIV-DYVHSQ RIV-DFHSQ RIV-DFHSQ RIV-TFAHSQ RIV-TFAHSQ RIV-TFAHSQ	-5
SEO 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 31 SEQ 35 SEQ 35 SEQ 35	2		TD- YHIAHL TP- WHMAHL TD- YHIAHL TD- YHLHL TD- YHLWHL TD- YHLWHL TD- YHLWHL TD- WHLWHL	GGIAORGPGL GGIAORGPGE GHLALKGAGL GGIAORGPGI GSLWARGPGI GSFAVRGPAL GSFALRGVPL YATMARGDWG GOFALHGTAL GAMGMRGFGL GOFALHGAAL GGIIORGPGL GSFAARGPGL GGIIORGPGL	MLIEATAVQP LMVEATAVEP VFIEATAVQP MHIEATSVSP TIVESTAVSP IILESIFVSE TIFFATGVLP LILIGNOVOT TIVEATSVTP VMVEATAVEA SMVEATAVQN IVTEVNAVSP IVTEVNAVSP IVTEVNAVSP	E-GRITPODV B-GRITPODU B-GRITPODU B-GRITPODU B-GRITPODU B-GCLSPHDL N-GRITPECS B-GCLSPHDL N-GRITPECS B-GRISPEDS R-GRISPEDS H-GRITPODV E-GRISPEDDV B-GRISPEDDV B-GRISPEDDV	GLMKDSGLMXDSGLMYDGGLMXDSGLMYDGGLMYDGGLMYDGGLMYDGGLMYDGGLMYDGGLMYDGGLMYDGGLMYDGGLMYDG	OLAPMR OLEPLE OLAPME	RVI-DPVHSQ RVI-EPVHSQ RVI-EPVHSQ RVI-DPVHSQ PIV-DYMSQ KIV-DPIHDQ KIV-DYIHSQ RIV-EPMSQ RIV-EPMSQ RIV-EPMSQ RIV-EPMSQ RIV-EPMSQ RIT-TFAHSQ	GO. KIGVQ NO. LIGVQ NO. LIGVQ GA. KVGIQ SO. KIGVQ DGICCIQ GO. KAGIQ GO. KAGIQ NO. VAGIQ NO. VAGIQ GO. KIAIQ GO. KIAIQ NO. VAGIQ GA. KIAIQ GA. KIAIQ
SEO 6 SEO 8 SEO 10 SEO 10 SEO 14 SEO 16 SEO 19 SEO 22 SEO 24 SEO 27 SEO 30 SEO 33 SEO 35 SEO 36 SEO 36 SEO 36 SEO 36 SEO 36	2		TD-YHIAHL TP-WHMAHL TD-YHIAHL TD-YHIAHL TD-YHLHY TD-WHLVHL TD-FHVVH TD-FHLVHL TD-FHLVHL TD-WHLVHL TD-WHLTHL TD-WHLTHL TD-WHLTHL TD-WHLTHL TD-WHLTHL TD-WHLTHL	GGIAORGPGL GGIAORGPGL GGIAORGPGL GHLALKGAGL GGIAORGPGL GSFAVRGPAL GSFALRGVPL YATHARGDWG GOFALHGTAL GOFALHGAAL GGIIORGPGL GSFAARGPGL GGIIORGPGL GGIIORGPGL	MLI EATAVQP LMVEATAVEP VFI EATAVQP MMI EATSVSP TIVESTAVSP TIVESTAVSP LILIGNVQLD TIVEATSVTP VMVEATAVSP SMVEATAVQN IVTEVNAVS P SMVEATAVTP	E-GRITPODV B-GRITPODV B-GRITPODV B-GRISPMDS B-GRITPODV B-GGLSPHDL N-GRISPEDS B-GRITPEDS B-GRISPEDS B-GRISPNDS B-GRISPNDS B-GRISPNDS B-GRISPNDS B-GRISPNDV B-GRISPNDV B-GRISPNDV B-GRISPNDV B-GRISPNDV B-GRISPNDV B-GRISPNDV		OLAPMR	RVI-DPVHSQ RVI-EPVHSQ RVI-EPVHSQ RVI-DPVHSQ RIV-DYHSQ RIV-DYHSQ RIV-DYHSQ RIV-DYHSQ RIV-EPHSQ RIV-TFHSQ RIV-TFHSQ RIV-TFHSQ RIV-TFHSQ RIT-TFAHSQ	GO. KIGVQ NO. LIGVQ NO. LIGVQ GA. KVGIQ SO. KIGVQ DGICCIQ GO. KAGIQ GO. KAGIQ NO. VAGIQ NO. VAGIQ GO. KIAIQ GO. KIAIQ NO. VAGIQ GA. KIAIQ GA. KIAIQ
SEO 6 SEO 8 SEO 10 SEO 10 SEO 12 SEO 14 SEO 16 SEO 19 SEO 24 SEO 24 SEO 27 SEO 30 SEO 33 SEO 35 SEO 36 SEO 40	2		TD- YHIAHL TP- WHMAHL TD- YHIAHL TD- YHIAHL TD- YHIAHL TD- YHIAHL TD- WHLVHL TD- WHLVHL TD- FHLVHL TD- FHLVHL TD- FHLVHL TD- TD- WHLVHL TD- WHL	GGIAORGPGL GGIAORGPGE GHLALKGAGL GHLALKGAGL GGIAORGPGL GSLWNRGPGI GSPALRGVPL GSPALRGVPL GAMGMRGPGL GOFALHGTAL GGIIORGPGL GGIIORGPGL GGIIORGPGL GGIIORGPGL	MLIEATAVOP LMVEATAVEP VFIEATAVOP MIEATSVSP TIVESTAVSP IILESIFVSE TIPEATGVLP TIPEATGVLP TIPEATGVLP TIPEATGVLP SMVEATAVEA SMVEATAVON IVTEVNAVSP SMVEATAVON TCVEATAVTP	E-GRITPODV B-GRITPODV B-GRITPODV B-GRITPODV B-GRITPODV B-GRITPODV N-GRITPECS N-GRISPEDS B-GRISPEDS R-GRISPEDV H-GRITPODV B-GRISPEDV C-GRISPEDV C-GRISPEDV C-GRISPEDV	GLMKDSGLMXDSGLMXDSGLMXDSGLMXDSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODSGLMODS	OLAPMR OLAPHA	RVI-DPVHSQ RVI-EPVHSQ RVI-EPVHSQ RVI-DPVHSQ PIV-DYAHSQ KIV-DPIHDQ RIV-DYIHSQ RIV-EPAHSQ RIV-EPAHSQ RIV-EFAHSQ RIT-TFAES RIT-TFAES RIT-TFAES RIV-EFAHSQ	GO-KIGV-O GO-KIGV-O GA-KVGI-O SO-KIGV-O GO-KIGI-O GO-KAGI-O GO-KIGI-O NO-KIGI-O SO-KIGI-O GO-KIGI-O SO-KIGI-O GO-KIAI-O GO-KIAI-O GO-KIAI-O GO-KIAI-O GO-KIAI-O GO-KIAI-O GO-KIAI-O GO-KIAI-O
SEO 6 SEO 8 SEO 10 SEO 12 SEO 14 SEO 16 SEO 22 SEO 24 SEO 27 SEO 30 SEO 31 SEO 35 SEO 38 SEO 42 SEO 42	2		TD- YHIAHL TP- WHMAHL TD- YHIAHL TD- YHIAHL TD- YHIAHL TD- YHIAHL TD- YHIAHL TD- HLYHL NN- PELAAV TD- PHLYHL TD- PHLYHL TD- FHLYHL TD- WHLTHL	GGIAORGPGL GGIAORGPGL GGIAORGPGL GGIAORGPGL GSLWNRGPGI GSFALRGYPL YATHARGDWG GOFALHGTAL GMGIORGFGL GOFALHGAL GGIIORGPGL GSFARGPGL GGIIORGPGL RRMQGGEWGO	MLIEATAVOP LMVEATAVEP LMVEATAVEP VFIEATAVOP MERATSVSP TIVESTAVSP TIVESTAVSP TIVESTAVSP TIVEATSVTP VMVEATAVSP SMVEATAVON TVTEVNAVSP SMVEATAVON TVTEVNAVSP SMVEATAVTP TCVEATAVTP	E-GRITPODV E-GRITPODV E-GRITPODV E-GRITPODV E-GRITPODV N-GRITPODV N-GRITPEDV N-GRITPEDV H-GRISPEDS E-GRISPEDS E-GRISPEDV H-GRITPODV E-GRISPEDA H-GRITPODV E-GRISPEDA H-GRITPODV E-GRISPEDA H-GRITPODV E-GRISPEDA E-GRISPEDA	-GLMK - DS -GLMK - DS -GLMC - DG -GLMC - DG -GLMC - DS -GLMC - DS -GLMC - DS -GLMC - DS -GLMC - DS -GLMC - DG -GLMC - DG -GLMC - DG -GLMC - DG -GLMC - DG -GLMC - DG -GLMC - DG	OLAPMR	RVI-DPVHSQ RVI-EPVHSQ RVI-EPHSQ RVI-DPVHSQ RIV-DPIHDQ RIV-DYIHSQ RIV-DYIHSQ RIV-DYIHSQ RIV-EPAHSQ RIV-TFAHSQ RIV-TFAHSQ RIT-TFAHSQ RIT-TFAHSQ RIT-TFAHSQ RIT-TFAHSQ RIT-TFAHSQ RIT-TFAHSQ RIT-TFAHSQ RIT-TFAHSQ RIT-TFAHSQ	GQ-KIGVQ NQ-LIGVQ NQ-LIGVQ NQ-LIGVQ SQ-KYGIQ GG-KYGIQ GG-KAGIQ GG-KAGIQ GG-KAGIQ GG-KIGIQ
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SEO 6 SEO 10 SEO 10 SEO 12 SEO 14 SEO 15 SEO 27 SEO 27 SEO 30 SEO 31 SEO 35 SEO 36 SEO 36 SEO 42 SEO 42 SEO 42 SEO 42 SEO 42 SEO 42 SEO 44 SEO 83 SEO 44 SEO 83 SEO 42 NP_625402 NP_625402 NP_259913 AT4675 AT4612 C02466 NC4452 SCOYEI SCOYEI SCOYEI	2		TD-YHIANL TP-WHMANL TN-YHLANL TN-YHLANL TD-YHIANL TP-YHLIPY TL-PHPYNT TD-WHLVHL PN-PELAVY TD-FHLVHL TD-YHLVHL TD-WHLTHL TD-WHLTHL TD-WHLTHL TP-WHCHL TP-WHCHL TM-WHCHL TM-WHCHL TM-WHCHL TM-WHCHL TM-WHCHL TP-YHIANL TP-FHLVHP TP-FHLVHP VPLFFVOEYY RG-DLMVQYY PNRDMAVEYY PNRDMAVEYY PNREMAVEYY PNREMAVEYY PNREMAVEYY PNREMAVEYY PNREMAVEYY PNREMAVEYY PNREMAVEYY PNREMAVEYY PNREMAVEYY	GIAORGPGL GGIAORGPGI GGIAORGPGP GHLALKGAGL GGIAORGPGP GHLALKGAGL GGIAORGPGI GSFANRGPGI GSFANRGPGI GSFANRGPGI GSPANRGPGI GGRACH G	MLIEATAVOP  MLIEATAVEP  VFIEATAVEP  VFIEATAVEP  VFIEATAVEP  TIVESTAVSP  TILESIPVET  TIPEATGVIP  LILTONVOVO  SIMPEATAVEA  SIMPEATAVEA  SIMPEATAVEA  SIMPEATAVEA  TOTANVHIDP  LOTANVHIDP  LOTEATAVEA  TOTANVHIDP  LOTEATAVEA  LOTEATAVEA  LOTEATAVEA  LOTEATAVEA  LOTEATAVEA  LOTEATAVEA  LITEATIPSE  LITEATIPSE  LOTEATERSE  LOTEATAVEA  LITEATIPSE  LOTEATIPSE  LO	E-GRITPODU B-GGLSPHIDL N-GRISPMDS B-GRITPODV B-GGLSPHIDL N-GRITPEDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRITPODV B-GRITPEDS B-GRITPODV B-GRITPEDS B-GRITPODL B-GRITPOD	-GLMK - DS -GLMK - DS -GLMG - DG -GLMG - DS -GLMG - DG	OJAPMR OJAPMR OJIPILS TTSEOPIGLK OAPKLK OAPKLK OAPKLK OIAPLK OIAP	RVI-DPVHSQ RVI-EPVHSQ RVI-EPVHSQ RVI-EPVHSQ RIV-DYJHSQ RIV-DYJHSQ RIV-DYJHSQ RIV-DYHSQ RIV-DFHSQ RIV-DFHSQ RIV-DFHSQ RIV-DFHSQ RIV-FFHSQ RIV-FFHSQ RIV-EFAHSQ LIV-EFAHSQ LIV-EFAHSQ R	GO - KIGVO GO - KIGVO GA - KVGIO GA - KVGIO GO - KIGVO GO - KIGVO GO - KIGVO GO - KIGIO GO -
SEO 6 SEO 10 SEO 12 SEO 12 SEO 14 SEO 15 SEO 15 SEO 16 SEO 24 SEO 27 SEO 30 SEO 31 SEO 31 SEO 31 SEO 31 SEO 31 SEO 38 SEO 40 SEO 40 SEO 40 SEO 40 SEO 41 SEO 42 SEO 48 SEO 85 Bacteria TAGES Bacteria TAGES	2		TD-YHIAHL TP-WHMAHL TN-YHLAHL TN-YHLAHL TD-YHIAHL TP-YHLIPY TC-PHEVPY TC-PHEVPY TC-PHEVPY TC-PHEVPY TC-PHEVPY TC-PHEVPY TC-PHEVPH TC-WHCHIL TC-WHCHIL TC-WHCHIL TC-WHCHIL TM-WHCHIL TM-WHCHIL TM-WHCHIL TM-WHCHIL TM-WHCHIL TC-FHEVH TC-FHEVH VPLEFVOEYY TC-PHEVPY TC-PHEV	GIAORGPGL GGIAORGPGI GGIAORGPGI GGIAORGPGI GHALKGAGI GGIAORGPGI GSFALKGYPL YATTAARGDWG GOFALHGTAL GAWARGPGL GGFALHGAAL GGIIORGPGL GGIIORGPGL GGIIORGPGL GGIIORGPGL GGIIORGPGL GGIAORGPGL GSFALHGVGN ASMARGGAGL GARAVGGTGL GARAVGGTGL GYALGAGL GGYALGAGL GGYALGAGL GGYALGAGL GGYALGAGL GGYALGAGL GGYALGAGL GGYALGAGL GGYALGAGL GGRAVPGTL TORAGNOTTH TORAGNPGTTL TORAGNPGTL TORAGNPGT	MLIEATAVOP  MLIEATAVEP  VFIEATAVEP  VFIEATAVEP  VFIEATAVEP  TIVESTAVSP  TILESIPVET  TIPEATGVIP  LILTONVOVO  SIMPEATAVEA  SIMPEATAVEA  SIMPEATAVEA  SIMPEATAVEA  TOTANVHIDP  LOTANVHIDP  LOTEATAVEA  TOTANVHIDP  LOTEATAVEA  LOTEATAVEA  LOTEATAVEA  LOTEATAVEA  LOTEATAVEA  LOTEATAVEA  LITEATIPSE  LITEATIPSE  LOTEATERSE  LOTEATAVEA  LITEATIPSE  LOTEATIPSE  LO	E-GRITPODU B-GGLSPHIDL N-GRISPMDS B-GRITPODV B-GGLSPHIDL N-GRITPEDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRISPMDS B-GRITPODV B-GRITPEDS B-GRITPODV B-GRITPEDS B-GRITPODL B-GRITPOD	-GLMK - DS -GLMK - DS -GLMG - DG -GLMG - DS -GLMG - DG	OJAPMR OJAPMR OJIPILS TTSEOPIGLK OAPKLK OAPKLK OAPKLK OIAPLK OIAP	RVI-DPVHSQ RVI-EPVHSQ RVI-EPVHSQ RVI-EPVHSQ RIV-DYJHSQ RIV-DYJHSQ RIV-DYJHSQ RIV-DYHSQ RIV-DFHSQ RIV-DFHSQ RIV-DFHSQ RIV-DFHSQ RIV-FFHSQ RIV-FFHSQ RIV-EFAHSQ LIV-EFAHSQ LIV-EFAHSQ R	GO - KIGVO GO - KIGVO GA - KVGIO GA - KVGIO GO - KIGVO GO - KIGVO GO - KIGVO GO - KIGIO GO -

App No.: NYA

Docket No.: HO-P03371US0 Inventor: Sandra E. Lavens et al. Title: 2031 OXIDOREDUCTASE

	201	211	221	231	241	251	261	271	281	291
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SEQ 3	LAHAGRKATT	VAPW	ISPS	ALATEKVGGW	PDRVKGPGDI	P	FAEPFAKP	KA	MTLDEIE	QPKK-DWVAA
SEQ 6	IAHAGRKAST	VAPW	LSAN	DTASEKMGGW LKADESVGGW	PARVKGPINV	PPUTP	PIVKNPVP	KB	MIKQDIE	DUKI-AWVAA
SEQ 8 SEQ 10	TAHACDKASA	TADW	- LAAQAGKSS	IVATEKVGGW	PORVIGESTV	P	FHETFPTP	KA	MTKDDIR	OPKR - DWFDA
SEQ 12	LGHGGRKASG	OPLF	LHLE	QVADKSVNGF	ADKAVAPSAL	A	FRPNGNLP	VPNE	LTKDEIK	RVVK-DFGAA
SEO 14	LNHAGRKIVE	GVPF		QQIQHGW	<b>OEHCVGPSTE</b>	P	FSDSHNTP	RB	LTVNEIN	SIVE-DFANA
SEQ 16	LAHAGRKAST	KAPW	HYQRGKS	ELAGPEOGGW	PENVWAPSAI	S	-YNEETFPFP	KB	MIVEQIH	ELVE-AWKAS
SEQ 19	INHPGROSPM	GAGT		RGLW	B-KAVAPSPV	P	-LVLGEAFVP	RLLSKVLFGT	PRELTVABIK	DIV-QKFAVT
SEQ 22	LAHAGRKAST	KAPWHDSPTP	SGEYKPREGL	QVVGPEYGGW	PDDVWAPSAI	P	FSEDFPNP	KE	MIVEEIE	GLVT-SFVDA
SEQ 24	LAHAGRKAST	TAPY	RG-Y	TVATEAQGGW	ENDVYGPFTN	B	DRWDENHAQP	HK	LTEKQYD	ELVD-KPVVA
SEQ 27 SEQ 30	LAHAGRKAST	UCDW	ITEARGK	ALAQESENGW AVAAEEVGGW	DONIVADEAT	λ	- OFNCUMBUR	KB	ETTE.SK	OURS-DAMES
SEQ 33	LISTAGRANAC	VSFM		AVAAEBVOON	PDNIVAPSAI	A	- QIMOTHETE	KA		Quico-Divini
SEO 35	IGHAGRKAST	VVPW	LDRK	NTAP?						
SEQ 38	LSHAGRKASC	VSPW	LSIN	AVAAKEVGGW	PDNIVAPSAI	A	-QEAGVNPVP	KA	FTKEDIE	ELKN-DFLAA
SEQ 40	LAHAGRKAST	VAPW	LSGG	DVAGEDVNGW	PODVWAPSAI	P	WNEKHAVP	KE	M\$LDDIE	AFKK-AFGEA
SEQ 42			LPS	KRAGKEAGGW	PEDVVGPSGG	EDFTWDERSS	SDPSGGYYAP	RE	LSVREIK	EMVQ-DWATA
SEQ 44	VGHPGRQARG	svQ	QHPISASD	VQLKQEM			FGSKFGVP	RP	ATKEDIK	AVIE-GFAHT
SEQ 83	IGHAGRKASC	VAPW	LDAG	LAAEKAAGGW KFVTQEEGGW	PDDVVGPSNE	P	FAPGYPTP	RA	ITLEELE	QLKE-DFVSG
SEQ 85 Bacteria	LAHAGRKASD	WSPF	TRGERRO	KPVIQEEGGW	PDRVVAPSAI	A	IAQGRVIP	KA	LITEDIN	KLQD-KFVQ3
T44612	TAHAGRKASA	NRPW	FGDD	HIGADDARGW	ETTAPSAT	A	PGAHLPNV	PRA	MTLDDIA	RVKO-DFVDA
NP 625402				APVGADAYGW						
NP_295913				GAVPAELGGW						
AF320254				IDEPLEAGAW						
OYE family										
Af4875				LISSS-AVPV						
Af4961	LWHAGRATIP	QMTG	SPAVSAS	ATVWDSPTEC	YSHPP	VGST	EPVRYADHPP	1E	LTIP-HL	KUTTRDYCNA
Ca2460 Nc4452	LWILGRVAND	ENT A	PAGLIPL	IGPSAVYW LKSSS-AVPM	PECAD		ALMAS VGNED	FF	BIEVEID	HIVEVETINA
ScOYE1	LWVICWAAFP	DNIA	REGGLR	YDSASDNVFM	DAEOR		AKAKKANNPO	HS	LTKDEIK	OYIK-EYVOA
ScOYE2	LWVLGWAAFP	DTLA	RDG-LR	YDSASDNVYM	NAEOB		EKAKKANNPO	HS	ITKDEIK	QYVK-EYVQA
ScOYE3	LWSLGWASFP	DVLA	RDG-LR	YDCASDRVYM	NATLQ		EKAKDANNLB	HS	LTKDDIK	QYIK-DYIHA
A36990	LWYLGRVANA	KDLK	DSG-LP	LIAPS-AVYW	DENSE		KLAKEAGNEL	RA	LTEEEID	HIVEVEYPNA
						251	261	221	201	201
	301	311	321			351		371	381	391
									8	
SEO 3									8	
SEQ 3 SEQ 6	TKRAIAA-GA	DFVEIHNAHG	YLLSSFLSP-		G-GSFENRIR	LSLEIAQLTR	DAVGPHVP	VFLR	ISAS-DWCE-	ETLPEQ
SEQ 6 SEQ 8	TKRAIAA-GA VKRAVKA-GA ARLAVQA-GV	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG	YLLSSFLSP- YLLMSFLSP- YLINEFLSP-	- AANNRTDQY - AVNTRTDEY - VTNKRTDAY	G-GSFENRIR G-GSFENRIR G-GSFENRTR	LSLEIAQLTR LSLEIAKLTR IVREVAAAIR	DAVGPHVP ENVPKDMP AVIPEGMP	VFLR VFLR	ISAS-DWCE- VSAT-DWLE- ISAT-EWLE-	ETLPEQ EVQPNKP -GQPVAAESG
SEO 6 SEO 8 SEO 10	TKRAIAA-GA VKRAVKA-GA ARLAVQA-GV CKRAIAA-GA	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG DFIEIHNAHG	YLLSSFLSP- YLLMSFLSP- YLINEPLSP- YLLSSFLSP-	- AANNRTDQY - AVNTRTDEY - VTNKRTDAY - SSNTRTDEY	G-GSFENRIR G-GSFENRIR G-GSFENRTR G-GSFENRIR	LSLEIAQLTR LSLEIAKLTR IVREVAAAIR LSLEIAQVTR	DAVGPHVP ENVPKDMP AVI PEGMP DAVGPNVP	VFLR VFLR LFLR	ISAS-DWCE- VSAT-DWLE- ISAT-EWLE- VSAT-DWIE-	ETLPEQ EVQPNKP -GQPVAAESG
SEQ 6 SEQ 8 SEQ 10 SEQ 12	TKRAIAA-GA VKRAVKA-GA ARLAVQA-GV CKRAIAA-GA ARRAVEISGF	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG DPIEIHNAHG DAVEIHGAHG	YLLSSFLSP- YLLMSFLSP- YLINEFLSP- YLLSSFLSP- YLINEFYSP-	-AANNRTDQY -AVNTRTDEY -VTNKRTDAY -SSNTRTDEY	G-GSFENRIR G-GSFENRIR G-GSFENRTR G-GSFENRIR G-GSFENRTR	LSLEIAQLTR LSLEIAKLTR IVREVAAAIR LSLEIAQVTR FLKEVIDSVK	DAVGPHVP ENVPKDMP AVIPEGMP DAVGPNVP SSIPNDVP	VPLRVPLRLPLRVPLR	ISAS-DWCE- VSAT-DWLE- ISAT-EWLE- VSAT-DWIE- ISAA-ENSP-	ETLPEQEVQPNKP -GQPVAAESGETLPEE
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14	TKRAIAA-GA VKRAVKA-GA ARLAVQA-GV CKRAIAA-GA ARRAVEISGF AWRAVEISKF	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG DPIEIHNAHG DAVEIHGAHG DAVEIHGAHG	YLLSSFLSP- YLIMSFLSP- YLINEFLSP- YLLSSFLSP- YLINEFYSP- CLIHOPLSK-	-AANNRTDQY -AVNTRTDEY -VTNKRTDAY -SSNTRTDEY -ISNKRTDEY -LINKRADQY	G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRTR G-GSFENRYR	LSLEIAQLTR LSLEIARLTR IVREVAAAIR LSLEIAQVTR FLKEVIDSVK FLLQIIENIK	DAVGPHVP ENVPKDMP AVIPEGMP DAVGPNVP SSIPNDVP RKIETP	VPLRLPLRVPLRVPLR	ISAS-DWCE- VSAT-DWLE- ISAT-EWLE- VSAT-DWIE- ISAA-ENSP- FPMS-DNCS-	ETLPEQEVQPNKP -GQPVAAESGETLPEE
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16	TKRAIAA-GA VKRAVKA-GA ARLAVQA-GV CKRAIAA-GA ARRAVEISGF AWRAVEISKF AQRALKA-GF	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG DPIEIHNAHG DAVEIHGAHG DAIEIHCANG DAIEIHCANG	YLLSSPLSP- YLIMSFLSP- YLINEPLSP- YLLSSFLSP- YLINEPYSP- CLIHQPLSK- YLISEFLSP-	-AANNRTDQY -AVNTRTDEY -VTNKRTDAY -SSNTRTDEY -ISNKRTDEY -LTNKRADQY -ISNORTDQY	G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR	LSLEIAQLTR LSLEIARLTR IVREVAAAIR LSLEIAQVTR FLKEVIDSVK FLLQIIENIK VLREIISAVR	DAVGPHVP ENVPKDMP AVIPEGMP DAVGPNVP RKIET P SVIPEDMP	VPLRLPLRVPLRVPLR	ISAS-DWCE- VSAT-DWLE- ISAT-EWLE- VSAT-DWIE- ISAA-ENSP- FPMS-DNCS- VSAT-EWME-	ETLPEQEVQPNKP -GQPVAAESGETLPEE
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19	TKRAIAA-GA VKRAVKA-GA ARLAVQA-GV CKRAIAA-GA ARRAVEISGF AWRAVEISKF AQRALKA-GF ARITAEA-GF	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG DFIEIHNAHG DAVEIHGAHG DAIEIHCANG DLIEIHAAHG NGVEIHAAHG	YLLSFLSP- YLIMSFLSP- YLIMEFLSP- YLINEFYSP- CLIHQFLSK- YLISEFLSP- YLLAQFLSK- YLLAQFLSK-	- AANNRTDQY - AVNTRTDEY - VTNKRTDAY - SSNTRTDEY - I SNKRTDEY - LTNKRADQY - LTNKRADQY - KTNRRGDEY	G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRVR G-GSFENRVR G-GSFENRTR	LSLEIAQLTR LSLEIAKITR IVREVAAAIR LSLEIAQVTR FLKEVIDSVK FLLQIIENIK VLREIISAVR IVGEIIKECR	DAVGPHVP ENVPKOMP AVIPEGMP DAVGPNVP SSIPNDVP RKIETP- SVIPEDMP RQVTEAVGEE	VFLRLFLRVPLR	ISAS - DWCE- VSAT - DWLE- ISAT - EWLE- VSAT - DWIE- ISAA - ENSP- FPMS - DNCS- VSAT - EWME- LNSA - DWQA-	ETLPEQ
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22	TKRAIAA-GA VKRAVKA-GA ARLAVOA-GV CKRAIAA-GA ARRAVEISGF AWRAVEISKF AORALKA-GF ARITAEA-GF AKRAIEA-GV	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG DAVEIHGAHG DAVEIHGAHG DAIEIHCANG DLIBIHAAHG NGVEIHAAHG DIIEIHGAHG	YLLSSFLSP- YLLMSFLSP- YLINEFILSP- YLINEFYSP- YLINEFYSP- CLIHQFLSK- YLISEFILSP- YLLAQFLSK- YLITEFILSP-	-AANNRTDQY -AVNTRTDEY -VTNKRTDAY -SSNTRTDEY -ISNKRTDEY -LTNKRADQY -ISNQRTDQY -KTNRRGDEY -LSNKRTDKY	G-GSFENRIR G-GSFENRIR G-GSFENRTR G-GSFENRTR G-GSFENRTR G-GSFENRTR G-GSFENRTR G-GSAENRAR G-GSFENRTR	LSLEIAQLTR LSLEIAKLTR IVREVAAAIR LSLEIAQVTR FLIKEVIDSVK FLLQIIENIK VLREIISAVR IVGEIIKECR VLIDIIKAVR	DAVGPHVP ENVPKDMP AVI PEGMP DAVGPNVP SSI PNDVP RKIETP- SVI PEDMP RQVTEAVGEE AVI PEEM	VFLRVFLRVFLR	ISAS - DWCE- VSAT - DWLE- ISAT - EWLE- VSAT - DWIE- ISAA - ENSP- FPMS - DNCS- VSAT - EWME- LNSA - DWQA- ISAT - EWME-	
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19	TKRATAA -GA VKRAVKA -GA ARLAVQA -GV CKRATAA -GA ARRAVEISGF AWRAVEISKF AQRALKA -GF AKRATEA -GV AKRAVEI -GV AKRAVEI -GF AKRANEI -GF AKRANEI -GF AKRANEI -GF	DFVEIHNAHG DFIEIHNAHG DFIEIHNAHG DFIEIHNAHG DAVEIHGAHG DAIEIHCANG DLIEIHAAHG MGVEIHAAHG DVIEIHGAHG DVIEIHGAHG DVIEIHGAHG	YLLSFLSP- YLIMSFLSP- YLINEFISP- YLINEFYSP- CLIHQFLSK- YLISEFLSP- YLLAQFLSK- YLITEFISP- YLLAGFLSK- YLISSTVSPA	- AANNRTDQY - AVNTRTDBY - VTNKRTDBY - SSNTRTDEY - ISNKRTDEY - LINKRADQY - ISNQRTDQY - KTNRRGDEY - LSNKRTDKY FTTNDRNDKY	G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRVR G-GSFENRVR G-GSFENRTR G-GSAENRAR G-GSFENRTR G-GSFENRTR	LSLEIAQLTR LSLEIAKLTR IVREVAAAIR FLKEVIDSVK FLLQIIENIK VLREIISAVR IVGEIIKECR VLIDIIKAVR FPMEVVHSVR	DAVGPHVP ENVPKDMP AVI PEGMP SSI PNDVP SKI ETP- SVI PEDMP RQUTEAVGBB AVI PEEM KAI PDSMP	VPLR VFLR VPLR VPLR VPLR VPLR LFVR LFVR EAKKFVVGIK LFYR	ISAS - DWCE- VSAT - DWLE- ISAT - EWLE- VSAT - DWI E- ISAA - ENSP- FPMS - DNCS- VSAT - EWME- LNSA - DWQA- ISAT - EWME- VTAT - DWLP-	
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30	TKRAIAA-GA VKRAVKA-GA ARLAVQA-GV CKRAIAA-GA ARRAVEISKF AWRAVEISKF AQRALKA-GF ARTITAEA-GF AKRAIEA-GV AKRAVEI-GF AKRAIKA-GF AKRAIKA-GF	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG DVIEIHGAHG DAVEIHGAHG DAIEIHCANG DLIEIHAAHG NGVEIHAAHG DVIEIHGAHG DVIEIHAAHG DVIEIHAAHG	YLLSSFLSP- YLIMSFISP- YLIMSFISP- YLIMSFISP- YLIMSFISP- YLIMSFISP- YLISEFISP- YLIAQFISK- YLITEFISP- YLISSTVSPA- YLLHQFISP- YLLHQFISP-	-AANNRTDQY -AVNTRTDEY -VTNKRTDAY -SSNTRTDEY -ISNKRTDEY -ISNKRTDEY -LINKRADQY -LINKRADQY -KTNRRGDEY -KSNKRTDKY -VSNQRTDEY	G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRUR G-GSFENRUR G-GSFENRUR G-GSFENRUR G-GSFENRUR G-GSFENRUR G-GSFENRUR	LSLEIAQLTR LSLEIAKLTR IVREVAAAIR LSLEIAQVTR FLKEVIDSVK FLLQIIENIK VLREIISAVR IVGEIIKECR VLIDIIKAVR FPMEVVHSVR	DAVGPHVP ENVP KDMP AVI PEGMP DAVGPNVP ST PNDVP RKI ET P - SVI PEDMP ROVTEAVGEE AVI PEEM KAI PDSMP	VFLRVFLR	ISAS - DWCE- VSAT - DWLE- ISAT - EWLE- VSAT - DWIE- ISAA - ENSP- FPMS - DNCS- VSAT - EWME- LNSA - DWQA- ISAT - EWME- VTAT - DWLP-	
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 33	TKRATAA-GA VKRAVKA-GA ARLAVQA-GV KKRATAA-GA ARRAVEISGF AWRAVEISGF AWRAVEISGF ARITAEA-GF ARITAEA-GF AKRAIEA-GV AKRAVEI-GF AKRAVEI-GF AKRANEA-GF AKRAIHA-GF	DFVEIHNAHG DFIEIHNAHG DVIEIHGAHG DAVEIHGAHG DAVEIHGAHG DAIEIHCANG DAIEIHCANG MGVEIHAAHG DVIEIHGAHG DVIEIHGAHG DVIEIHAAHG DVIEIHAAHG	YLLSSPLSP- YLLMSFLSP- YLLMSFLSP- YLLMSFLSP- YLLMSFLSP- YLLMSFLSP- YLLAGPLSK- YLLTEPLSP- YLLAGPLSK- YLLTEPLSP- YLLAGPLSP-	-AANNRTDOY -AWNTRTDEY -VTNKRTDAY -VTNKRTDAY -SSMTRTDEY -ISNKRTDEY -LINKRADOY -KTNRRGDEY -LSNKRTDKY -KTNRRGDEY -LSNKRTDKY -VSNQRTDEY -VSNQRTDEY	G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GTFERRIL	LSLEIAQUTR LSLEIAQUTR LSLEIAQVTR FLKEVIDSVK FLLQIIENIK VURBIISAVR IVGBIIKECR VLIDIIKAVR VLIDIIKAVR	DAVGPHVP ENVPKDMP AVIPEGMP DAVGPNVP SSIPNDVP RKIETP- SVIPEDMP ROVTEAVGEE AVIPEEM AAIPETTP	VPLR VFLR VPLR VPLR VPLR LFVR EAKKFVVGIK LFVR EAVER LFYR VFYR	ISAS - DMCE- VSAT - DMLE- ISAT - EWLE- ISAT - EWLE- ISAT - EWLE- ISAA - ENSP- FPMS - DNCS- VSAT - EWME- LNSA - DWQA- ISAT - EWME- VTAT - DWLP- VSAT - DWFEF	ETLPEQEVOPNKP
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 33 SEQ 33	TKRAIAA-GA VKRAVKA-GA ARLAVQA-GA ARRAVEISGF AWRAVEISKF AGRALKA-GF ARITAEA-GF AKRAIEA-GV AKRAVEI-GF AKRAIAA-GF	DFVEIHNAHG DFIEIHNAHG DFIEIHNAHG DVIEIHGAHG DAIEIHCANG DAIEIHCANG DLIEIHAAHG MGVEIHAAHG DVIEIHAAHG DVIEIHAAHG DVIEIHAAHG	YLLSSPLSP- YLLMSFLSP- YLLMSFLSP- YLLSSFLSP- YLLSSFLSP- YLLSSFLSP- YLLAOPLSK- YLLAOPLSK- YLLSSTVSPA YLLHOPLSP-	-AANNRTDOY -AVMIRTDEY -AVMIRTDEY -VINKRTDEY -ISNKRTDEY -ISNKRTDEY -ISNKRTDEY -INKRADOY -KINRRDEY -KINRRDEY -KINRRDEY -VSNORTDEY -VSNORTDEY -TDEY	G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRUR G-GSFENRUR G-GSFENRUR G-GSAENRAR G-GSAENRAR G-GSFENRIR G-GSFENRIR	LSLEIAQLTR LSLEIAKLTR LSLEIAKLTR LSLEIAQVTR PLKEVIDSVK PLLQIIENIK VLREIISAVR IVGEIIKEVR VULBIIKAVR FPMEVVHSVR	DAVGPHVP ENVPKOMP AVI PESMP DAVGPNVP SSI PNDVP SVI PEDMP RQVTEAVGEE AVI PEEM KAI PDSMP AAI PETTP		ISAS - DMCE- VSAT - DMLE- ISAT - BMLE- ISAT - BMLE- VSAT - DWIE- ISAA - EMSP- PFMS - DMCS- VSAT - EMME- LNSA - DWQA- ISAT - EMME- VTAT - DWLP- VSAT - DWFEF	
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SEÓ 6 SEO 8 SEO 10 SEO 12 SEO 14 SEO 16 SEO 19 SEO 22 SEO 24 SEO 30 SEO 33 SEO 35 SEO 38 SEO 38	TRRAIAA-CA VKRAVKA-GA ARLAVQA-GV CKRAIAA-GA ARRAVEISKF AQRALKA-GF AKRAIEA-GF AKRAIEA-GF AKRAIEA-GF AKRAIEA-GF AKRAIEA-GF AKRAIEA-GF KRAIEA-GF KRAIEA-GF KRAIA-GF KRAIA-GF KRAIA-GF KRAIA-GF	DFVEIHNAHG DFISIHNAHG DFISIHNAHG DVISIHGAHG DFISIHNAHG DAVEIHGAHG DAISIHCANG DLISIHAAHG MGVSIHAAHG DVISIHAAHG DVISIHAAHG DVISIHAAHG DVISIHAAHG DVISIHAAHG DVISIHAAHG DVISIHAAHG	YLLSSPLSP- YLLMSFLSP- YLLMSFLSP- YLLNEFLSP- YLLNEFYSP- YLLAGPLSK- YLLTEPLSP- YLLAGPLSP- YLLHGPLSP- YLLHGPLSP- YLLHGPLSP- YLLHGPLSP-	-AANNRTDQY -AVMIRTDEY -VTNKRTDAY -SSMIRTDEY -ISNKRTDEY -ISNKRTDEY -ISNKRTDEY -ISNKRTDKY -ISNKRTDKY -ISNKRTDKY -ISNKRTDKY	G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRUR G-GSFENRUR G-GSFENRUR G-GSAENRAR G-GSAENRAR G-GSAENRAR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR G-GSFENRIR	LSLEIAQLTR LSLEIAYLTR LSLEIAYLTR LSLEIAQVTR PLKEVIDSVK VLREIISAVR VLREIISAVR VLREIISAVR VLDIIKAVR FPMEVVHSVR  VVLEILDLIR VVLEILLIR LTMESRRPCP	DAVGPHVP ENVPKDMP AV1 PEGMP DAVGPNVP SSI PNDVP SVI PEDMP SVI PEDMP KAI PDSMP AAI PETTP		ISAS - DMCE- VSAT - DMLE- ISAT - BMLE- VSAT - DMLE- VSAT - DMLE- VSAT - DMS- VSAT - EMME- LISAA - DMCS- VSAT - EMME- VTAT - DMLP- VSAT - DMFEF	ETLPEQEVQPNKP -GQPVAAESGETLPER
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SEO 6 SEO 10 SEO 10 SEO 12 SEO 14 SEO 16 SEO 16 SEO 19 SEO 27 SEO 27 SEO 30 SEO 30 SEO 35 SEO 38 SEO 42 SEO 42 SEO 44 SEO 83 SEO 42 SEO 83 SEO 83 SEO 83 SEO 83 SEO 84 SEO 84 SEO 84 SEO 84 SEO 85 Bacteria T44612 NP_235913 AFF320254 OVE family Af4875 Af4961 Ce2460	TKRATAA-GA VKRAVKA-GA ARLAVGA-GV CKRATAA-GA ARRAVELSGP AMRAVELSGP AKRALKA-GP AKRALEA-GV AKRAVELSGP AKRATEA-GV AKRAVELSGP AKRATEA-GV AKRAVELSGP AKRATHA-GP	DFVEINNAHG DVIEINAHG DVIEINAHG DVIEIHAHG DVIEIHAHG DAVEIHGAHG DAIEHCAHG DLIEIHAHG DLIEIHAHG DVIEIHAHG DVIEHAHG	YLLSSPISP- YLLMSFISP- YLLMSFISP- YLLMSFISP- YLLSSFISP- YLLSSFISP- YLLAOPISP- YLLAOPISP- YLLAOPISP- YLLHOPISP- YLLHOPISP- YLLHOPISP- YLLHOFISP- YLLMSFISP- YLLMSFISP- YLLMSFISP- YLLMSFISP- YLMSFISP- YLLMSFISP- YLMSFISP- YLMSFI	AANNRTOOY ANVIRTOEY VINKRTDAY VINKRTDAY VINKRTDAY ISNKHTDEY LINKRADOY ISNORTDOY ISNORTDOY ISNORTDOY VINGREDEY VINGREDEY VINGREDEY VINGREDEY VINGREDEY ANTORTDEY TITNORTDEY LINGREDEY LINGREDEY LINGREDEY LINGREDEY LINGREDEY LINGREDEY LINGREDEY LINGREDEY LINGREDEY SCHERODRE NVMKRTDAY LANGREDEY ASNKRTDAY LANGREDEY SCHERODRE NVMKRTDEY TORREDEY	G-GS FENRIR	LSLEIAQLTR LSLEIAVLTR IVREVAAAIR LSLEIAVLTR FLKEVIDSVK VLREIISAVR IVGBI IKAVR VULBILISAVR VVLBILISAVR VVLBILILII LTHESREPCP LLIBIVTAVR LILEVTAVR FLLEVTAVR FLLEVTAVR FLLEVVAAVR LLLEVVAAVR FLLEVVAAVR FLLEVVAAVR FLLEVVAAVR FLLEVVAAVR FLLEVVAAVR FLLEVVAAVR FLLEVVAAVR FLLEVVAAVR FLLEVVAAVR FLLEVIAMBILA FALEVVAAVR FLLEVIAMBILA FALEVVAAVR FALEVVAAVR FALEVVAAVR FLLEVIAMBILA FALEVVAAVR FALEVAR FALEVVAAVR FALEVVAR FALEVAR FALEVVAR FALEVAR FALEVVAR FALEVAR FALE	DAVGPHYP- DAVGPHYP- AVIPEGMP- AVIPEGMP- SSIPNDYP- SSIPNDYP- SSIPNDYP- SVIPEDMP- KAIPCHONE AVIPEDMP- AAIPETTP- AAMPSSMP- AAMPSSMP- RRTSKNF- AAWPEDMP- QEPPNKG- EVWPDDRP- HVWPAHLD- AMMPTNRP- EAVGADR- ATYGEDN- GIVGAEK- EAVGAEK- EAVGAEK- EAVGAEK- EAVGAEK-	VPLR VPLR VPLR VPLR IPVLR LPVR CAMPACA LPVL LPVR LPVR LPVR LPVR LPVR LPVR LPVR	ISAS DWCE- ISAS DWCE- ISAT- DWLE- ISAT- DWLE- ISAT- DWLE- ISAT- DWLE- ISAT- DWS- ISAT- D	
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	401	411	421	431	441	451	461	471	481	491
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SEQ 3	SWKSEDTVR-	FAQELVK Q	GAVDLIDISS	GGVLAQQ	KI	KSGPAFQVPP	AVAVKKAVGD	KLLVAAV	GAIT	
SEQ 6	SWRGVDTVR-	- FAKILA-BT	GYVDVLDVSS	GGTHSEQ	ні	HAKPGFQAPP	A I AVKNAVGD	KLAVASV	GMIA	
SEQ 8	SWDM-QSSL-	ELVKKLPB	WGIDLVDVSS	AANHKDQ	XI	NLHTAYQTDL	AGQIRQAI	RAAGAST	LVGAVGLITD	SEQARGLVQG
SEQ 10	SWKLSDSVR-	FAEALAA Q	GAIDLIDVSS	GGVHAAQ	KI	KSGPAPQAPP	AVAIKKAVGD	KLLVATV	GTIT	
SEQ 12		-LADILVE								
SEQ 14	AWSTEDALK-	-LADLVID ELAKILPD	LCVKVIDVIS	CCNNVIDO	KILLIND	DECENSORS	ARREASHIRN	RCLIACS	GLUTSA	RIAKETVOEK
SEQ 16 SEO 19		-QIELFEQ								
SEQ 22		-LAKLLPD								
SEO 24	GWEIEDTVAP	TLAARLR D	GGVDLIDVSS	GGNHKDQ	RI	EVKDCYQVPF	ARKI KDQVNG	ILLGAV	GMIR	
SEQ 27										
SEQ 30										
SEQ 33	SWIVEQTC	QLARILPK	HGVDLVDVSS	GGIHPKS	AIAI	KSGPAYQVDL	AKQVKKAVGD	SVLVSAV	GGIK	
SEQ 35										
SEQ 38										
SEQ 40 SEO 42		-ISKILAD								
SEO 44		LCEALEAAGM								
SEQ 83		-LAHQLA D								
SEQ 85	SWIVDOTVE-	LAKMLOB	ARVDLLDVSS	GGLVPPQ	KI	TVGAGYQLFG	AKAVRDALAK	I EPDASKR	MLVGA	
Bacteria										
T44612	EQTLEESI	ELARRPKA	GGLDLLSVSV	GFTIPET	NI	PWGPAFMGPI	AERVRREAKL	PVTSAW	GFGT	
NP_625402	GWT PDDTVR -	-FARDLEA	HGIDLLDVST	GGNVPRV	RI	PTGPGYQVPP	AARVKAGST-	LPVAAV	GLIT	
NP_295913	GWDLEQTVQ-	-LSKLLKY	ECVDVLDISS	GGLTAAQ	01	EVGPGYQVPP	AAAVSRAETE	ISVMAV	GLIE	
AP320254	GNTADDAVA-	-IARLFKE	AGADIIDCSS	GQVWKGD	QP	VYGRMYQTPP	ADRIRNEVGI	PTLAVG	AISE	
OYE family	m unompy	LIAQM	DDI DUNYI UI	ANCOM		PYDUDDDNUP	VENDVAC - 0 -	CC-DILLA	CCVD	
Af4875 Af4961	EUD-ALGLEI	LCESLKKAHP	NI-SVUSE	TEDDAE		-ULESVEEKD	NFLRSWG	LSDVDLSSFR	KIRGTTPEES	
Ca2460	ERIHSY	ILQQLQQRAD	NGOOLAYVSI.	IEPRVIG	TFDASI.	EDOKGRSNEF	AYKYWKG	NFVRA	GNYT	
Nc4452	DLIPOFED	VIRKIN	-GFGLAYLHL	TOSRVAGN	MDVQP	EEDEE-NLAP	AAKLWDG	PLLIA	GGLT	
ScOYE1	ETGIVAQYAY	VAGELEKRAK	AGKRLAFVHL	VEPRVTNP	FLTEGE	GEYEGGSNDF	VYSIWKG	PVIRA	GNFA	
SCOYE2	<b>ETGIVAQYAY</b>	VLGELERRAK	AGKRLAFVHL	VEPRVTNP	FLTEGE	GEYNGGSNKP	AYSIWKG	PIIRA	GNFA	
ScOYE3	<b>EPGIIAQYSY</b>	VLGELEKRAK	AGKRLAFVHL	VEPRVTDP	SLVEGE	GEYSEGTNDP	AYSIWKG	PIIRA	GNYA	
A36990	EEIHSY	ILQQLQQRAD	NGQQLAYISL	VEPRVTG	IYDVSL	KDQQGRSNEF	AYKIWKG	NFIRA	GNYT	
	501	611	521	521	541	551	561	571	581	591
	501	511	521					571	581	591 1
									1	1
SEQ 3	NGKQAN	QILEEQD			IDVALVG	RGFQKDPGLA	WTFAQHLGV-			QIRWGFTRRG
SEQ 6	NGKQAN	QILEEQD			IDVALVG	RGFQKDPGLA RGFQKNPGLV	WTFAQHLGV- WAWADELNV-		EISMAN	QIRWGFTRRG QIRWGFSRRG
SEQ 6 SEQ 8	NGKQAN SAHLANS ADEATAAEAM	QILEEQD LLEKDG LSGPEPK			IDVALVG LDLVLVG	RGFQKDPGLA RGFQKNPGLV RQFLREPEWV	WTFAQHLGV- WAWADELNV- FSTARKLGV-			QIRWGFTRRG QIRWGFSRRG QFGRAI
SEQ 6 SEQ 8 SEQ 10	NGKQAN SAHLANS ADEATAAEAM NGKQAN	QILEEQD LLEKDG LSGPEPK KLLEEEG			IDVALVG LDLVLVG ADAILIA	RGFQKDPGLA RGFQKNPGLV RQFLREPEWV RGFQKDPGLA	WTFAQHLGV- WAWADELNV- FSTARKLGV- WTFAQHLDV-			QIRWGFTRRG QIRWGFSRRG QIRWGFSRRG QFGRAI QIRWGFTRRG
SEQ 6 SEQ 8 SEQ 10 SEQ 12	- NGKQ AN SAHLANS ADEATAAEAM - NGKQ AN	QILEEQD LLEKDG LSGPEPK KLLEEEG KYLEEGT			IDVALVGLDLVLVGADAILIALDVALVG	RGFOKDPGLA RGFOKNPGLV ROFLREPEWV RGFOKDPGLA RGFLRNPGLV	WTFAQHLGV- WAWADELNV- FSTARKLGV- WTFAQHLDV- WEFADKLGV-		1EISMANEISMANPVTVPVEIAMAS	QIRWGFTRRG QIRWGFSRRG QFGRAI QIRWGFTRRG QLGWGFWPNK
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14	- NGKQ AN SAHLANS ADEATAAEAM - NGKQ AN KDPELLN RD I FKLD	QILEEQD LLEKDG LSGPEPK KLLEEGG KYLEEGT EFIANGD			IDVALVGLDLVLVGADAILIALDVALVGFDLALIG	RGFOKDPGLA RGFOKNPGLV ROFLREPEWV RGFOKDPGLA RGFLKNPGLV KGFLKNTGLI	WTFAQHLGV- WAWADELNV- FSTARKLGV- WTFAQHLDV- WEFADKLGV- SRIADQLQA-			QIRWGFTRRG QIRWGFSRRG QFGRAI QIRWGFTRRG QIRWGFWPNK QYKLALS
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16	- NGKQAN - SAHLANS ADEATAAEAM - NGKQAN - KDPELLN - RDIFKLD E-DGRVTIOR	QILEEQD LLEKDG LSGPEPK KLLEEG KYLEEGT EFIANGD ENGAKTR			IDVALVGLDLVLVGADAILIALDVALVGFDLALIGFDLALIGFDIALIG	RGFOKDPGLA RGFOKNPGLV ROFLREPEWV RGFOKDPGLA RGFLKNPGLV KGFLKNTGLI ROFLKEPEFV	WTFAQHLGV- WAWADELNV- FSTARKLGV- WTFAQHLDV- WEFADKLGV- SRIADQLQA- LTVADELGV-			QIRWGFTRRG QIRWGFSRRG QFGRAI QIRWGFTRRG QLGWGFWPNK QYKLALS QYLRGPLSSR
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19	NGKQANSAHLANS ADEATAAEAMNGKQANKDPELLNRDIFKLD E-DGRVTIQRTRQGME	QILEEQD LLEKDG LSGPEPK KLLEEGG KYLEEGT EPIANGD AALESDD			IDVALVGLDLVLVGADAILIALDVALVGFDIALIGFDIALIG	RGFOKDPGLA RGFOKNPGLV ROFLREPEWV RGFOKDPGLA RGFLKNYGLV KGFLKNYGLV ROFLKEPEFV RPAI INPSLP	WTFAQHLGV- WAWADELNV- PSTARKLGV- WTFAQHLDV- WEFADKLGV- SRIADQLQA- LTVADELGV- ANLILNPEV-		1EISMAN	OIRWGFTRRG OIRWGFSRRG OFGRAI QIRWGFTRRG OLGWGFWPNK QYKLALS QYLRGPLSSR LFDKKRAEPH
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16	NGKQANSAHLANS ADEATAAEAMNGKQAN	QILEEQD LLEKDG LSGPEPK KILLEEGG EYLEEGT EPIANGD ENGAKTR AALESDD DVVDEQGAEK EILESGK	VAEAKQTHDT	IEVVSESHGG	IDVALVGLDLVLVGADAILIALDVALVGFDLALIGFDIALIGADMVLVACDMIGIG KTKADLVLIAADVTFVA	RGFQKDPGLA RGFQKNPGLV RQFLREPEWV RGFQKDPGLA RGFLRNPGLV KGFLKNTGLI RQFLKEPEFV RPAI INPSLP RQFLREPEFV REPLRNPSLV	WTFAQHLGV- WAWADELNV- FSTARKLGV- WTFAQHLDV- WEFADKLGV- SRIADQLQA- LTVADELGV- ANLI LNPEV- LRTAHNLGV- LDSANQLGE-			1
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22	NGKQANSAHLANS ADEATAAEAMNGKQANKDPELLNRDIFKLD E-DGRVTIQRTRQGMETADIARDGLFITAN	QILEEQD LLEKDG LSGPEPK KYLEEGG KYLEEGT EPIANGD ENGAKTR AALESDD DVVDEQGAEK EILESGK	VAEAKQTHDT	IEVVSESHGG	IDVALVGLDLVLVGADAILIALDVALVGFDLALIGFDLALIGADMVLVACDMIGIG KTKADLVLIAADVTFVA	RGPOKDPGLA RGFOKNPGLV ROFILREPEWV RGFOKDPGLA RGFILKNTGLI ROFILKEPEFV RPAI INPSLP ROFILREPEFV REPLENPSLV	WTFAQHLGV- WAWADELNV- FSTARKLGV- WTFAQHLDV- WEFADKLGV- SRIADOLQA- LTVADELGV- ANLILINPEV- LRTAHNLGV- LDSANQLGE-			1
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30	- NGKQAN SAHLANS ADEATAAEAM - NGKQAN KDPELLIN - RDIFKLD E - DGRVTIQR TRQGME - TADI - AR - DGLFTTAN	QILEEQD LLEKDG LSGPEPK KYLLEEGG KYLEEGT EPIANGD EPIANGD ENGAKTR AALESDD DVVDEQGAEK EILESGK	VAEAKQTHDT	IEVVSESHGG	IDVALVGLDLVLVGADAILIALDVALVGFDLALIGFDLALIGADMVLVACDMIGIG KTKADLVLIAADVTFVA	RGFOKDPGLA RGFOKNPGLV ROFLREPEWV RGFOKDPGLA RGFLRNPGLV KGFLKNTGLI ROFLKEPEFV RPAI INPSLP ROFLREPEFV REFLRNPSLV	WTFAQHLGV- WAWADELNV- FSTARKLGV- WTFAQHLDV- WEFADKLGV- SRIADQLQA- LIVADELGV- ANLI LNPEV- LRTAHNIGV- LDSANQLGE-			OIRWGFTRRG OIRWGFSRRG OFGRAI OIRWGFTRRG OLGWGFWPNK OYKLALS OYLRGPLSSR LFDKKRAEPH OYHRAVWRKG OYDYAVKGHR
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 33	- NGKQ - AN SAHLANS ADEATAREAM - NGKQ - AN - KDPELLN - RDI FKLD E - DGRYTIOR - TROGME - TADI - AR - DGLFTTAN - TGHL - AE	QILEBOD LLEKDG LSGPEPK KYLEEGG KYLEEGT EPIANGD ENGAKTR AALESDD DVVDEQGAEK EILESGK EVLQSG	VAEAKOTHDT	IEVVSESHGG	IDVALVGLDLVLVGADAILIALDVALVGFDIALIGFDIALIGFDIALIGADMYLVACDMIGIG KTKADLVLIAADVTFVA	RGFOKDPGLA RGFOKDPGLA RGFOKDPGLA RGFLKNPGLV KGFLKNTGLI ROFLKEPEFV RPAIINPSLP ROFLREPEFV RPAINPSLV RWFOONPGLV	WTPAQHLGV- WARMADELNV- FSTARKLGV- FSTARKLGV- WTPAQHLDV- WEFADKLGV- SRIADQUOA- LITVADELGV- ANLILNPEV- LRTAHNLGV- LGSANQLGE- LGSANQLGE-		EISMAN EISMAN PYTYPY EIAMAS RLHOAL OFRTAP DVKAPV PDADAR NVOWPH NVAWPV	QIRWGFTRRG QIRWGFSRRG QIRWGFSRRG QIGWGFWPNK QYKLALS QYLRGFLSSR LFDKKRAEPH QYHRAVWRKG QYDYAVKGHR
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 33 SEQ 33 SEQ 35	- NGKQ - AN - SAHLANS ADEATAAEAM NGKQ - AN - KUPELLN - RDIFLLN E - DGRVTIQR - TRQOME - TADI - AE - DGLFTTAN	QILEEQD QILEERQD LLEKNG LSGPEPK KYLEEGG KYLEEGT EPIANGD ENGAKTR AALESDD DVVDEQGAEK EILESGK EVLQSG	VAEAKOTHDT	IEVVSESHGG	IDVALVGLDIVINGLDVALVG	RGFOKDPGLA RGFOKDPGLA RGFOKDPGLA RGFLRNPGLV KGFLKNTGLI ROFLKEPBFV RPAI INPSLP ROFLREPBFV REFLRNPSLV	WTPAQHLGV- WARADELMV- FSTARKLGV- WTPAQHLDV- WEPAQKLGV- SRIADOLQA- LTVADELGV- ANLILNPEV- LRTAHNLGV- LDSANQLGE- RAPANELGV-			OIRMGFTRRG OIRMGFSRRG OFGRAI OIRMGFTRRG OLDMGFMPNN OYLAGIS-SR LFDKKRAEPH OYHRAWRKG OYHRAWRKG OYHRAWRKG
SEQ 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 33 SEQ 33 SEQ 38	- NGKQ- AN - SAHLANS ADEATMARAM - NGKQ- AN - NCDPELLN - RDIFFKLD E DORVTIOR - TROOME - TADI - AR - DGLFTTAN - TCHL- AE	QILEEQD LLEKDG LSGPEPK KLLEEGG EFIANGD ENGAKTR AALESDD DVVDEQGAEK EILESGK EVLQSG	VAEAKOTHDT	IEVVSESHGG	IDVALVGLDIAVIVGLDIAVIVGLDVALVGFDIALIGFDIALIGFDIALIGCDMTGIG KTKADLVLIAADVTFVA	RGFOKDPGLA RGFOKNPGLV RGFOKDPGLA RGFLKNPGLA RGFLKNPGLI ROFLKEPEFV ROFLREPEFV REPLRNPSLV REPLRNPSLV	WTFAQHLGV- WARADELNV- FSTARKLGV- WTFAQHLDV- WEFADKLGV- SRIADOLGA- LTVADELGV- SRIADOLGA- LTVADELGV- LATHANIGV- LDSANQLGE- RAPANELGV-		EISMAN EISMAN PVTVPV EIAMAS EIAMAS CHCTAP DVKAPV PDADAV NVOWPH NVAWPV	QIRWGFTRRG QIRWGFSRRG QIRWGFSRRG QIRWGFTRRG QULWGFWPNK QYLLALS
SEO 6 SEQ 8 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 24 SEQ 27 SEQ 30 SEQ 33 SEQ 35 SEQ 38 SEQ 40	- NGKQ AN - SAHLANS ADEATAAEAM - NGKQ AN - NGPELIN - RDIFKLD - RDIFKLD - TROGME - TADI AR - DGLFTTAN - TCHL AE	QILEEQD LLEKDG LSGPEPK KLLEEGG KYLEEGT EFIANGD ENGAKTR AALESDD EVVDEQGAEK EILESGK	VAEAKOTHDT	IEVVSESHGG	IDVALVGLDIVINGLDIVINGLDVALVG	RGFOKDPGLA RGFOKDPGLA RGFLREPEMV RGFOKDPGLA RGFLRNPGLV RGFLKEPEFV ROFLKEPEFV ROFLREPEFV REFLRNPSLV RWFOONPGLV	WTFAQHLGV- WARADELMV- FSTARKLGV- WTFAQHLDV- WEFADKLGV- SKIADOLOA- LTVADELGV- LTVADELGV- LATTAHNLGV- LDSANQLGE- RAPANELGV-		EISMAN EISMAN EISMAN EVTYPV EIAMAS RIHGAL OPERTAP DVKAPV PDADAP NVOWPH NVAWFV	OIRMGFTRRG OIRMGFSRRG OIRMGFSRRG OIRMGFTRRG OIRMGFTRRG OYKLALS- OYKLRGLSSR LFPKKRAEPH OYHRAVWKKG
SEQ 6 SEQ 8 SEQ 10 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 22 SEQ 24 SEQ 30 SEQ 30 SEQ 35 SEQ 35 SEQ 35 SEQ 35 SEQ 42 SEQ 42	- NGKQ- AN - SAHLANS ADEATAABAM - NGKQ- AN - NGPELIN - RDIFKLD - RDIFKLD - TGOME - TADI - AR - DGLFTTAN - TGHL- AE	QILEEQD LLEKDG LSGFEPK KILEEEG EFIANGD ENGAKTR AALESDD DVVDEQGAEK EILESGK EVLQSG	VAEAKOTHDT	IEVVSESHGG	IDVALVGLDLVIVGLDLVIVGLDLVIVGADATLIALDVALVGFDLALIGFDIALIGFDIALIGADMYLVACDMIGIG KTKADLVLIAADVTFVAADVTFVA	RGPOKDPGLA RGFOKNPGLV RGFOKDPGLA RGFLRNPGLV KGFLKNTGLI ROPLKEPEFV RPAI INFSLP ROFLEEFFV REPLRNPSLV REPLRNPSLV	WTPAQHLGV- WARADELNV- FSTARKLGV- WTPAQHLDV- WEPADKLGV- SRIADQLQA- LTVADELGV- LTVADELGV- LATAHNLGV- LDSANQLGE- RAPANELGV-		EISMAN EISMAN FYTVPV EIAMAS RIHGAL OFRTAP DVKAPV PDADAR NVOWPH NVAWPV	OIRMGFTRRG OIRMGFRRG OFGRAI OIRMGFFRRG OYGLALS OYGLALS OYLLGOLS R LFFXKRAEPH OYHRAWRKG OYHRAWRKG
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SEQ 6 SEQ 8 SEQ 10 SEQ 10 SEQ 12 SEQ 14 SEQ 16 SEQ 19 SEQ 22 SEQ 22 SEQ 24 SEQ 30 SEQ 30 SEQ 35 SEQ 35 SEQ 35 SEQ 35 SEQ 42 SEQ 42	-NGKO-AN -SAHLANS ADEATAAEAM -NGKQ-AN -NGKQ-AN -NDIFKLD -RDIFKLD -TRQOME -TADI-AE -TGHL-AE -TGHL-AE -VGAM-VDA -IGTL-AE -VGAM-VDA	QILEEOD- QILEEOD- LLIEKDG- LSGPEPK- KILEEEG- KYLEEGT- EFIANGD- ENGAKTR- AALESDD- DVVDEOGAEK EILESGK-  BVLQSG- LQGVDG- LQGVDG- EIIAGG- SYDSPNG-	VAEAKOTHDT	I EVVSESHGG	IDVALVGLDIVLVGADAILIALDIVALVGADAILIALDIVALVGFDIALIGFPIALIGFPIALIGADMYLIAADVIFVAIDIVRAGIDIVRAGIDIVRAGIDIVRAG	RGPOKDPGLA RGPOKDPGLA RGPOKDPGLA RGPLRNPGLV RGPLRMTGLI RGPLRMTGLI RGPLRMTGLI ROFLKEPEF RPAIINPSLV RWFQONPGLV RWFQONPGLV RAAGSEPDLA RLPGKNTGLV KLAEOSIOSS	WTPAOHLGV WAWADELNV PSTARKLGV WTPAQHLDV SRIADQLOA LITVADELGV ANLILINFEV LITVADELGV ANLILINFEV LDSANQLGE RAPANELGV KDIIAGKVSS WSWADDLNT SCODAVLLAR	I IKYAMGEDE		OIRMGFTRRG OIRMGFTRRG OIRMGFRRG OIRMGFTRRG OIRMGFTRRG OYKLALS OYKLALS OYKRAEPH OYKRAEPH OYKRAEPH OHRAWRKG OYHAWRKG OHRAWRKG OHRAWRKG OIRMGFKGRG
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SED 6 SED 10 SED 12 SED 12 SED 14 SED 16 SED 16 SED 19 SED 22 SED 27 SED 27 SED 30 SED 30 SED 30 SED 35 SED 36 SED 42 SED 42 SED 42 SED 42 SED 42 SED 44 SED 85 Bacteria T44612 NP_235913 AFF320254 OYE family Af4875	- NGKO - AN - SAHLANS ADEATAAEAM - NGKO - AN - KOPELLAN - RDI FKLD - DOL FKLD - TROOME - TADI - AR - DOLFTTAN - TCHL - AE - VGAM - VDA - IGFL - AE - VGAM - CDA - TGA - QAE - TGA - QAE - TGA - QAE - TGA - QAE - AD - HAN	QILEEQD- LLEKDG- LSGPPK- KILLEEGG- KYLEEGT- EPIANGD- EPIANGD- EPIANGD- EVIAGGAEK- AALESDD- DVVDEQGAEK EILESGK EVIQSG EVIQSG EVIQSG EVIQSG EVIQSG EVIAGGG- SYDSPNG AALQANQ KILANGE- AILQAGD- SIIAAGR- SIIAAGR-	VAEAKOTHDT	I EVVSESHGG	- IDVALVG - ADATLIA - LDVALVG - POIALIG - POIALIG - POIALIG - ADMVLVA - CDMNGIG - ADMVLVA - IDIVRAG - IDIVRAG - IGIG DTPLDLVASG - ODRSOIG - LDLVSVG - ADMVLIG - ADLTAIG - ADLTAI	RGFOKDPGLA RGFOKDPGLA RGFOKDPGLA RGFIKEPEMV RGFIKEPEMV RGFIKEPEFV RGFIKEPEFV RPAI INFSLP RMFOONPGLV RAAGSEPDLA RLFOKNTGLV KLABOSIOSG RAHLADPHMA RPHLADPHMA RPHLADPHMA	WTFAQHLGV WTFAQHLGV WTFAGHLDV WEFADKLGV SRIADQUOA LITVADELGV ANLILINEV LDSANQLGE RAPANELGV KDIIAGKVSS KODIIAGKVSS WSWADDLNT ECDAVLLAR YFAAKELGV QHARRELGU QHARRELGU QHARRELGU LHEBAKIGF	IIKYAMGEDE GLMSYPS	- EISMAN - EISMAN - PYTTYP - EIAMAN - PYTTYP - EIAMAN - PYTTYP - PIAMAN - PYADAN - NVOWPH - NVAWFY - EVKMAN - SIGIAH WTEDASVALM - EKASWT - DARMPD - RPVSID - GEVAWP - GEVAWP - GEVAWP	OIRMGFTRRG OIRMGFRRG OFGRAI OIRMGFMPNK OYKLALS OYKLALS OYKLALS OYKLALS OYKLAUS OY
SED 6 SED 10 SED 12 SED 12 SED 12 SED 12 SED 16 SED 19 SED 22 SED 24 SED 27 SED 30 SED 30 SED 30 SED 30 SED 30 SED 30 SED 42 SED 43 SED 43 SED 44 SED 83 SED 42 SED 83 SED 44 SED 84 SED	- NGKO - AN - SAHLANS ADEATAAEAM - NGKO - AN - KOPELLAN - RDI FKLD - DOL FKLD - TROOME - TADI - AR - DOLFTTAN - TCHL - AE - VGAM - VDA - IGFL - AE - VGAM - CDA - TGA - QAE - TGA - QAE - TGA - QAE - TGA - QAE - AD - HAN	QILEEQD- LLEKDG- LSGPPK- KILLEEGG- KYLEEGT- EPIANGD- EPIANGD- EPIANGD- EVIAGGAEK- AALESDD- DVVDEQGAEK EILESGK EVIQSG EVIQSG EVIQSG EVIQSG EVIQSG EVIAGGG- SYDSPNG AALQANQ KILANGE- AILQAGD- SIIAAGR- SIIAAGR-	VAEAKOTHDT	I EVVSESHGG	- IDVALVG - ADATLIA - LDVALVG - POIALIG - POIALIG - POIALIG - ADMVLVA - CDMNGIG - ADMVLVA - IDIVRAG - IDIVRAG - IGIG DTPLDLVASG - ODRSOIG - LDLVSVG - ADMVLIG - ADLTAIG - ADLTAI	RGFOKDPGLA RGFOKDPGLA RGFOKDPGLA RGFIKEPEMV RGFIKEPEMV RGFIKEPEFV RGFIKEPEFV RPAI INFSLP RMFOONPGLV RAAGSEPDLA RLFOKNTGLV KLABOSIOSG RAHLADPHMA RPHLADPHMA RPHLADPHMA	WTFAQHLGV WTFAQHLGV WTFAGHLDV WEFADKLGV SRIADQUOA LITVADELGV ANLILINEV LDSANQLGE RAPANELGV KDIIAGKVSS KODIIAGKVSS WSWADDLNT ECDAVLLAR YFAAKELGV QHARRELGU QHARRELGU QHARRELGU LHEBAKIGF	IIKYAMGEDE GLMSYPS	- EISMAN - EISMAN - PYTTYP - EIAMAN - PYTTYP - EIAMAN - PYTTYP - PIAMAN - PYADAN - NVOWPH - NVAWFY - EVKMAN - SIGIAH WTEDASVALM - EKASWT - DARMPD - RPVSID - GEVAWP - GEVAWP	OIRMGFTRRG OIRMGFRRG OFGRAI OIRMGFMPNK OYKLALS OYKLALS OYKLALS OYKLALS OYKLAUS OY
SED 6 SED 10 SED 12 SED 12 SED 14 SED 16 SED 16 SED 19 SED 22 SED 27 SED 27 SED 30 SED 30 SED 30 SED 35 SED 36 SED 42 SED 42 SED 42 SED 42 SED 42 SED 44 SED 85 Bacteria T44612 NP_235913 AFF320254 OYE family Af4875	-NGKO - AN -NGKO - AN -NGHANS ADEATAAEAM -NGKO - AN -NGPELIN -EDIFKILD -DGRVTIOR -TROOME -TADI - AR -DGLFTTAN -TGHL - AE -VGAM - VDA -IGTL - AE -VGAM - EG -VGAM - EG -VGAM - EG -TADI - AR	QILEEOD- LLEKDG- LLEKDG- LSGPPPK- KILLEEG- EFIANGD- EFIANGD- ENGAKTR AALESDD- DVVDEOGAEK EILESGK EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG EVLOSG SYDS PNG AALQANO KILANGE AALQANO KILANGE AALQANO KILANGE SIIAAGR SIIAAGR MAAATYT GVLEEGR LHDLOND DREPPEK	VAEAKOTHDT	I EVVSESHGG  ED	- IDVALVG - ADATLIA - LDVALVG - ADATLIA - LDVALVG - FDIALIG - FDIALIG - FDIALIG - FDIALIG - FDIALIG - COMMIGIG KTRADLVLIA - ADVTFVA - IDIVRAG - IDIVRAG - DTPLDLVASG - DTPLDLVASG - ADLALAG - ADLALAG - ADLALAG - ADLALAG - ADLALAG - YDALLYG - TIVGFR - DVVATFR - LDVATFR	RGFOKDPGLA RGFOKDPGLA RGFOKDPGLA RGFIKNPGLV RGFLKNPGLV RGFLKNPGLV RPAIINSLP RPAIINSLP REFLRNPSLV RAAGSEPDLA RLFOKNTGLV KLAEOSIOSG RAHLADPHMA REILRNPSMA RPFLRDPHMA RPFLRDPHMA RYFISTDLP RYFTSNPDLV RFFISNPDLV RFFISNPDLV	WTPAQHLGV WTPAQHLGV WTPAQHLDV WTPAQHLDV WTPAQHLDV WTPAQHLDV WTPAQHLGV SRIADOLQA LTVADELGV ANLILNEV LDSANQLGE  KDIIAGKVSS KDIIAGKVSS WSWADDLNT ECDAVLLAR YFFAKELGV QHAARELGU LHERAKIGF FRYMAGIQL LHERAKIGF EKLRKGIPF EKLKIGFPI	IIKYAMGEDEGLMSYPS	- EISMAN - EISMAN - EISMAN - PVTVPV - EIAMAS - RLHQAL - OFRTAP - DVKAPV - PDADAR - NVOWPH - NVAWPV - SVKMAN - SIQIAH - WTEDASVALM - EKASWT - DARMPD - GEVAWP - OKURAP - GEVAWP - OKURAP	OIRMGFTRRG OIRMGFSRRG OFGRAI OIRMGFTRRG OYKLAIS OYKLAIS OYKLAIS OYKRAWRKG OYHRAWRKG OYHRAWRKG OYHRAWRKG OYHRAWRKG OHRAWRKG OHRAWRKG OHRAWRKG CHAMARGER OIRMARGER OIRMARGER OIRMARGER OIRMARGER OIRMARGER OIRMARGER OIRMARGER OIRMARGER FYTAHMLE OYGNGM OYRAGM KOYRSARGOY SFYSTLSREG EFYKYNY-G TFYKAKSPO
SED 6 SED 10 SED 12 SED 12 SED 11 SED 15 SED 16 SED 16 SED 19 SED 22 SED 27 SED 27 SED 30 SED 30 SED 30 SED 35 SED 36 SED 42 SED 42 SED 44 SED 83 SED 44 SED 85 Bacteria T44612 C2460 NC4452 SCOYEI	NGKO-AN - SAHLANS ADEATAAEAM - NGKO-AN - SAHLANS ADEATAAEAM - NGKO-AN - KOPELLN - TRODIFKLD - TRODIFKLD - TADI-AC - TADI-AC - TADI-AC - TADI-AC - VGAM-VDA - TGTL-AC - VGAM-VDA - TGTL-AC - VGAM-GG - TGA-QAC	OILEGOD- LIEROG- LIGEPOG- LSGEPEK- KULEEGG- KYLEEGT- EFIANGD- ENGAKTR- AALESDD- DVVDEQGAEK EILESGK LOGVDG- EVLOSG SYDSPNG AALQANO- KILANGG SYDSPNG AALQANO- KILANGG SILAGG SILAGG SILAGG SILAGG SILAGG	VAEAKOTHDT	I EVVSESHGG  ED  ED	IDVALVG ADATLIA LDVALVG PDIALIG PTILIG	RGFOKDPGLA RGFOKNPGLAV ROFLREPENV RGFOKDPGLA RGFLKNPGLAV RGFLKNPGLAV RGFLKNPGLAV RGFLKNPGLAV ROFLREPEV ROFLREPEV REPLRNPSLAV	WTFAQHLGV WTFAQHLGV WTFAQHLDV WFFAQHLDV WFFAQHLDV WFFAQHLDV WFFAQHLDV WFFAQHLGV ANLILINPEV LDSANQLGE LTTAHNIGV LDSANQLGE KDIIAGKVSS KDIIAGKVSS KOLIAGKVSS KOLIAGKVSS CHARRELGV QHARRELGV QHARRELGV QHARRELGV GRARRELGV FFRYMAGIQL ERLEKGIPF FFYMAGIQL ERLEKGIPF FFRYMAGIQL FRIKEGIPL FRIKEGIPL	I IRYAMGEDEGLMSYPS		OIRMGFTRRG OIRMGFRRG OFGRAI OIRMGFRRG OFGRAI OIRMGFRRG OLGMGFMPNN OYKLALS OYKLAGPIN OYKLAGPIN OYKAGPIN OYKAGPIN OYKAGPIN OYKAGPIN OYKAGPIN OYKAGPIN OYKAGPIN OIRMARGER OIRMARGER OIRMARGER OIRMGFGGA GTRAAGNPOY LPAPYAHMLE OYARAGW- OYARAGW- OYARAGW- SFYSTLSRED RFYGFFEDNA FFYKYNYN-G TFYKARSPDG
SED 6 SED 10 SED 10 SED 12 SED 12 SED 12 SED 16 SED 19 SED 22 SED 24 SED 24 SED 27 SED 30 SED 30 SED 31 SED 31 SED 31 SED 42 SED 44 SED 83 SED 42 SED 44 SED 83 SED 42 SED 44 SED 83 SED 42 SED 83 SED 42 SED 84 SED 83 SED 44 SED 83 SED 42 SED 84 SED 83 SED 44 SED 83 SED 42 SED 84 SED 85 BACTETIA T44612 NP_255913 AF720254 OVE family Af4875 Af4961 Cc2460 NC4452 SCOYEL	-NGKO-AN -NGKO-AN -NGKO-AN -SAHLANS ADEATAAEAM -NGKO-AN -NGPELLN -EDIFKLD -DGRVTIOR -TROOME -TADI-AR -DGLFTTAN -TGHL-AE -VGAM-VDA -VGAM-VDA -VGAM-VDA -TGHL-AE -VGMM-EG -POLAE -POLAE -TGA-QAE -	QILEEOD- LLEKDG- LLEKDG- LSGPPPK- KILEEEG- KYLEEGT- EPIANGD- EPIANGD- ENGAKTR- AALESDD- DVVDEOGAEK EILESGK- EVLOSG- EVLOSG- EVLOSG- EVLOSG- EVLOSG- EVLOSG- EVLOSG- SYDS PNG- AALQANQ- KILANGE- AALQANG- KILANGE- AALQANG- KILANGE- AALQANG- KILANGE- CVLEEGR- LHDLDND- DREFPEK- REEVKDP-	VAEAKOTHDT	I EVVSESHGG  ED	- IDVALVG - ADATLIA - DVALVG - PDIALIG - FDIALIG - FDIALIG - FDIALIG - FDIALIG - TDIALIG - TDIALIG - TDIALIG - ADMYLVA - CUMIGIG - TDIVRAG - TGIG - TGIG - DTPLDLVASG - ODRSOIG - LDLVSVG - ADAVILIG - ADLCAIA - ADLCAIA - NVAIAPG - TYDALLYG - TTVGFG - TTUGFG - TTLIGYG - TTLIGYG - TLIGYG - TLIG	RGPOKDPGLA RGPOKNPGLV ROFLREPEWV RGPOKDPGLA RGPLKNPGLV RGPLKNPGLV RGPLKNPGLV ROFLKEPEFV RPAINSLP RAGSEPDLA RAGSEPDLA RLPOKNTGLV KLAEOSIOSG RAHLADPHMA RELLRNPSMA RELLRNPSMA RYFISTDLP RYFTSNPLV RFFTSNPLV RFFTSNPLV RFFTSNPDLV	WTPAQHLGV WTPAQHLGV WTPAQHLDV FSTARKLGV WTPAQHLDV SRIADOLQA LTVADELGV ANLILINEV LDSANQLGE LRTAHNLGV LDSANQLGE KDIIAGKVSS KAPANELGV CHARACLGV QHAARELGV QHAARELGV QHAARELGL LHEAAKIGF FRVMAGIQL ERLEKGIPE EKLKIGFPE EKLKIGFPE EKLKIGFPE DRIEKGLPL DRIEKGLPL DRIEKGLPL DRIEKGLPL DRIEKGLPL	I IKYAMGEDEGLMSYPS		OIRMGFTRRG OIRMGFRRG OFGRAI OIRMGFTRRG OYLLAIS OYLL
SED 6 SED 10 SED 12 SED 12 SED 11 SED 15 SED 16 SED 16 SED 19 SED 22 SED 27 SED 27 SED 30 SED 30 SED 30 SED 35 SED 36 SED 42 SED 42 SED 44 SED 83 SED 44 SED 85 Bacteria T44612 C2460 NC4452 SCOYEI	NGKO-AN - NGKO-AN - SAHLANS ADEATAAEAM - NGKO-AN - SAHLANS ADEATAAEAM - NGKO-AN - RDIFKLD - TRODME - TADI-AC - TADI-AC - TADI-AC - TADI-AC - TADI-AC - VGAM-VDA - TGTL-AC - VGAM-VDA - VGAM-VDA - TGTL-AC - VGAM-VDA - TGTL-AC - VGAM-VDA - VGAM	OILEGOD- LIEROG- LIGEPOG- LSGEPEK- KULEEGG- KYLEEGT- EFIANGD- ENGAKTR- AALESDD- DVVDEQGAEK EILESGK LOGVDG- EVLOSG SYDSPNG AALQANO- KILANGG SYDSPNG AALQANO- KILANGG SILAGG SILAGG SILAGG SILAGG SILAGG	VAEAKOTHDT	I EVVSESHGG  ED  ED	IDVALVG ADATLIA LDVALVG PDIALIG PTLIGYG	RGFOKDPGLA RGFOKNPGLAV ROFLREPENV ROFLREPENV RGFOKDPGLA RGFLKNPGLAV RGFLKNPGLAV RGFLKNPGLAV ROFLREPETV RPAINNPSLAV REPLRNPSLAV RAGSSEPDLA RLFOKNTGLAV KLAEDSIOSG RAHLADPHMA RYPISTPDLP RYPTSNPDLAV RYPTSNPDLAV RHFISTPDLP RYPTSNPDLAV RHFISTPDLP RFFISNPDLAV RFFIS	WTPAQHIGU WTPAQHIGU WTPAQHIDU LITAHNIGU LITAHNIGU LITAHNIGU LITAHNIGU LITAHNIGU LITAHNIGU LITAHNIGU LITAHNIGU LITAHNIGU RAPANELGU QHAMRELGU QHAMRELGU QHAMRELGU QHAMRELGU QHAMRELGU GHAMRELGU GHAMRELGU GHAMRELGU GHAMRELGU GHAMRELGU GHAMRELGU HERAMKIGF FRYMAGIQL ERILKIGI PE FRIKEGI EL GRILKIGG PE FRIKEGI EL DRILEKGI PL DRILEKGI	I IRYAMGEDEGLMSYPS	- EISMAN - EISMAN - PYTTYPY - EIAMAS - RIHGAL - OFRTAP - DVKAPV - PDADAR - NVOWPH - NVAWPY - STOLLTACSA - SIGIAH WTEDASVALM - EKASWT - DARMPD - RPVSID - GEVAWP - QKVDRA - TPVDRS - NHYDRD - NKYDRD - NKY	OIRMGFTRRG OIRMGFRRG OFGRAI OIRMGFRRG OFGRAI OIRMGFRRG OLGMGFMPNN OYKLALS OYKLAGENS OYKLAGENS OYKAGENS OYKRAGENS OYKRAGENS OIRMGFRGGA OIRMGFRGGA GTRAAGNPOY LPAPYAHMLE OYAWAGH OYAWAGH EFYKYNY-G FFYKSAG-G TFYMSAB-G

	601	611	621	631
SEQ 3		KQSIFDV		
SEQ 6	AGPYLRKKLE	KI		
SEQ 8				
SEQ 10	GTPYIDPKAY	KESIFE		
SEQ 12	QQIVDLIERT	SKLEVN		
SEQ 14				
SEQ 16	PKKLTTVP			
SEQ 19	WIVEKLGMKS	<b>IVGAGVEVTW</b>	YVSELKKLAK	F
SEQ 22	ARI			
SEQ 24	KLR			
SEQ 27				
SEQ 30				
SEQ 33	KKVNKSSL			
SEQ 35				
SEQ 38				
SEQ 40				
SEQ 42				
SEQ 44	PFDI SNADEV	ARVTQLMAEG	KV	
SEQ 83	KKNAPKLVL-			
SEQ 85	HRVHVAKK			
Bacteria				
T44612	RYR			
NP_625402				
NP_295913				
AF320254	ETNLORAAAA	VAGK		
OYE family				
Af4875	YLDYPPSAEY	MALHNPPV		
Af 4961	KCYVDYPPAT	ASS		
Ca2460	YNSYDESEKQ	VIGKPLV		
Nc4452	YIDOPPSKEP	EKVYGAQA		
ScOYE1	YIDYPTYEEA	LKLGWDKK		
ScOYE2	YIDYPTYEEA	LKLGWDKN		
SCOYE3	YTDYPTYEEA	VDLGWNKN	••	
A36990	YNSYDESEKQ	VIGKPLA		

Figure 1. A multiple alignment of the 2031 OR amino acid sequence from A. fumigatus (SEQ ID No3) along with related 2031 ORs from other fungi and bacteria (see Example 4) and OYEs. Regions 1-11, marked with \* or #, refer to amino acids conserved between ORs but not OYEs.

Fungal 2031 ORs are given by the following SEQ ID No.: A. fumigatus, SEQ ID Nos. 3, 6 and 8; A. nidulans, SEQ ID No. 10; C. albicans SEQ ID Nos. 12 and 14; N. crassa, SEQ ID Nos. 16 and 19; M. grisea SEQ ID Nos. 22 and 44; S. pombe SEQ ID No. 24 (NP\_595868); C. trifolii SEQ ID No. 27; F. sporotrichioides SEQ ID Nos. 30, 33 and 35; F. graminearum SEQ ID Nos. 38 and 83; M. graminicola SEQ ID Nos. 40 and 42; U. maydis SEQ ID No 85.

Bacterial ORs resembling 2031 are: T44612 (Pseudomonas putida), SEQ ID No. 86; NP\_625402 (Streptomyces coelicolor), SEQ ID No. 87; NP\_295913 (Deinococcus radiodurans), SEQ ID No. 88; AF320254 (Azoarcus evansii, SEQ ID No. 89.

Fungal ORs similar to the Old Yellow Enzyme family (originally identified in *S. cerevisiae*):

A. fumigatus, Af4875 and Af4961, SEQ ID Nos. 90 and 91 respectively; C. albicans, Ca2460 and A36990, SEQ ID Nos. 92 and 93 respectively; N. crassa, Nc4452, SEQ ID No. 94; S. cerevisiae, OYE1, OYE2 and OYE3, SEQ ID Nos. 95-97 respectively.

Details of the sequence searches that identified the ORs other than SEQ ID No. 3, and methods for the construction of multiple alignments are given in Example 4 hereinafter.

App No.: NYA
Docket No.: HO-P03371US0
Inventor: Sandra E. Lavens et al.
Title: 2031 OXIDOREDUCTASE

	1	11	21	31	41	51	61	71	81	91
SEQ 1			TTCGACCCAA							
SEQ 2										
SEQ 4 SEQ 5										
SEQ 7										
SEQ 9										
SEQ 11 SEQ 13										
SEQ 15										
SEQ 17										
SEQ 18										
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SEQ 34 SEQ 36										
SEQ 37										
SEQ 39										
SEQ 41 SEQ 43										
SEQ 82										
SEQ 84										
	101	111	121	131	141	151	161	171	181	191
SEQ 1	CAGTGCCCTT	CCCGAATGA	CTGTCTCCAC			CAAGCCTGAA			AGTCGTATGT	
SEQ 2									GTATGT	TCTACTGATT
SEQ 4										
SEQ 5 SEQ 7										
SEQ 9										
SEQ 11										
SEQ 13 SEQ 15										
SEQ 17										
SEQ 18										
SEQ 20 SEQ 21										
SEQ 23										
SEQ 25								CGAAA	CCTCGACCCA	AACAAACAGC
SEQ 25 SEQ 26								CGAAA	CCTCGACCCA	AACAAACAGC
SEQ 25								CGAAA	CCTCGACCCA	AACAAACAGC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32								CGAAA	CCTCGACCCA	AACAAACAGC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTT	ATAAATACCT	ATACTTGTTT	GTTCACTTCT	CCTCGACCCA	AACAAACAGC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTTT	ATAAATACCT	ATACTTGTTT	GTTCACTTCT	ATGCTACTCA	AACAAACAGC GAAC TATCAATCCG
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTTT	ATAAATACCT	ATACTTGTTT	GTTCACTTCT	CCTCGACCCA	AACAAACAGC GAAC TATCAATCCG
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTTT	ATAAATACCT	ATACTTGTTT	GTTCACTTCT	CCTCGACCCA	AACAAACAGC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTTT	ATAAATACCT	ATACTTGTTT	GTTCACTTCT	ATGCTACTCA	AACAAACAGC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 36 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTTT	ATAAATACCT	ATACTTGTTT	GTTCACTTCT	ATGCTACTCA	AACAAACAGC GAAC TATCAATCCG
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTTT	ATAAATACCT	ATACTTGTTT	GTTCACTTCT	ATGCTACTCA	AACAAACAGC GAAC TATCAATCCG
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTTT	ATAAATACCT	ATACTTGTTT	CGAAA	ATGCTACTCA	AACAAACAGC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82	AGGAAG	TTGCATGTCA	CTTGTAGTGA	CAGGGCGTCG	TGTAAATTTT	ATAAATACCT	ATACTTGTTT	CGAAA	CCTCGACCCA ATGCTACTCA ATGCTACTCA 281	AACAAACAGCGAAC TATCAATCCG
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84	AGGAAG	TTGCATGTCA  211  GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	CAGGGCGTCG  231  AAAGATCACC AAAGATCACC	TGTAAATTTT 241 GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GTITCTTACC GTITCTTACC	ATACTTGTTT  261  AACCCATCAA  AACCCATCAA	CGAAA	CCTCGACCCA ATGCTACTCA 281 CAATCTCCTA CAATCTCCTA	AACAAACAGCGAAC TATCAATCCG
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84	AGGAAG	TTGCATGTCA  211  GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	CAGGGCGTCG  231  AAAGATCACC AAAGATCACC	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GTTTCTTACC GTTTCTTACC	ATACTIGITI  261  AACCCATCAA AACCCATCAA	GITCACTTCT  271  TAACCATCCA TAACCATCCA	CCTCGACCCA ATGCTACTCA 281 CAATCTCCTA CAATCTCCTA CAATCTCCTA CAATCTCCTA	AACAAACAGCGAAC TATCAATCCG
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84	AGGAAG	TTGCATGTCA  211  GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	CAGGGCGTCG  231  AAAGATCACC AAAGATCACC	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GTTTCTTACC GTTTCTTACC	ATACTIGITI  261  AACCCATCAA AACCCATCAA	GITCACTTCT  271  TAACCATCCA TAACCATCCA	CCTCGACCCA ATGCTACTCA 281 CAATCTCCTA CAATCTCCTA AATCTCCTA	AACAAACAGCGAAC TATCAATCCG
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 82 SEQ 84	201 TCTGTGCCTG	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	CAGGGCGTCG  231  AAAGATCACC AAAGATCACC	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GTTTCTTACC GTTTCTTACC	ATACTTGTTT  261  AACCCATCAA AACCCATCAA	CGAAA  GITCACTTCT  271  TAACCATCCA TAACCATCCA	CCTCGACCCA ATGCTACTCA 281 CAATCTCCTA CAATCTCCTA CAATCTCCTA AAAAAAAA	AACAAACAGC TATCAATCCG TATCAATCCG TATCAATCCG TATCAAAAAT CAACAAAAAT TGTCGCAACC TGTCGCAACC TGTCGCAACC TGTCGCAACC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 37 SEQ 37 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 82 SEQ 84	201 TCTGTGCCTG	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	231 AAAGATCACC	TGTAAATTTT 241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GTTTCTTACC GTTTCTTACC	ATACTTGTTT  261  AACCCATCAA AACCCATCAA	CGAAA	CCTCGACCCA ATGCTACTCA 281 CAATCTCCTA CAATCTCCTA A A A A A A A A A A A A A A A A A A A	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 82 SEQ 84	201 TCTGTGCCTG	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	CAGGGCGTCG  231  AAAGATCACC AAAGATCACC	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GITTCTTACC GITTCTTACC	ATACTIGITT  261  AACCCATCAA AACCCATCAA	CGAAA  GTTCACTTCT  271  TAACCATCCA TAACCATCCA	ATGCTACTCA  281  CAATCTCCTA CAATCTCCTA AAATCTCCTA AAATCTCCTA AAATCTCCTA AAATCTCCTA AAATCTCCTA AAATCTCCTA AAATCTCCTA AAATCTCCTA AAAATCTCCTA AAAAATCTCCTA AAAAATCTCCTA AAAAATCTCCTA AAAAATCTCCTA AAAAAAAA	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 82 SEQ 84 SEQ 2 SEQ 4 SEQ 5 SEQ 7 SEQ 9 SEQ 11 SEQ 13 SEQ 13 SEQ 13 SEQ 15 SEQ 17	201 TCTGTGCCTG	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	231 AAAGATCACC	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GITTCITACC GITTCITACC	ATACTIGTT  261  AACCCATCAA  ACCCATCAA	271 TAACCATCCA TAACCATCCA	ATGCTACTCA  281  CAATCTCCTA  CAATCTCCTA	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 82 SEQ 84 SEQ 82 SEQ 84 SEQ 15 SEQ 15 SEQ 15 SEQ 13 SEQ 13 SEQ 11 SEQ 13 SEQ 15 SEQ 17 SEQ 11 SEQ 15 SEQ 17 SEQ 18 SEQ 17 SEQ 18 SEQ 17 SEQ 18 SEQ 17 SEQ 18 SEQ 17 SEQ 18 SEQ 18 SE	201 TCTGTGCCTG	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	CAGGGCGTCG  231  AAAGATCACC AAAGATCACC	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GITTCTTACC GITTCTTACC	ATACTTGTTT  261  AACCCATCAA AACCCATCAA	GTTCACTTCT  271  TAACCATCCA TAACCATCCA	ATGCTACTCA  ATGCTACTCA  CAATCTCCTA CAATCTCCT	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 82 SEQ 84 SEQ 2 SEQ 4 SEQ 5 SEQ 7 SEQ 9 SEQ 11 SEQ 13 SEQ 13 SEQ 13 SEQ 15 SEQ 17	201 TCTGTGCCTG	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	231 AAAGATCACC	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GTTTCTTACC GTTTCTTACC	ATACTTGTTT  261  AACCCATCAA  AACCCATCAA	CGAAA	ATGCTACTCA  281  CAATCTCCTA CAATCTCCTA A A A A A A A A	AACAAACAGC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 34 SEQ 37 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 1 SEQ 2 SEQ 84 SEQ 1 SEQ 2 SEQ 1 SEQ 2 SEQ 1 SEQ 2 SEQ 1 SEQ 2	201 TCTNGTGCCTG TCTGTGCCTG	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	231 AAAGATCACC AAAGATCACC	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA	ATAAATACCT  251  GITTCTTACC GITTCTTACC	ATACTTGTTT  261  AACCCATCAA AACCCATCAA	271 TAACCATCCA TAACCATCCA	281  CAATCTCCTA CAATCT	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84  SEQ 1 SEQ 2 SEQ 4 SEQ 1 SEQ 2 SEQ 1 SEQ 2 SEQ 1 SEQ 2	201 TCTGTGCCTG TCTGTGCCTG TCTGTGCCTG TCTGTGCCTG	211  GCGCAGACGG GCGCAGACGG CTTGACAACAC	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT AAGCCGGCCA	231 AAAGATCACC AAAGATCACC TCCTCGCCGA	TGTAAATTTT  241  GCACCGAGGA GCACCGAGGA CCCGAGGA CCCGAGGA CCCGAGGA CCCGAGGA CCCGAGGA	ATAAATACCT  251  GTITCTTACC GITTCTTACC TACCCCGGCA	ATACTTGTTT  261  AACCCATCAA AACCCATCAA TAGTCACACT	271 TAACCATCCA TAACCATCCA CGCACGTCCCC	CCTCGACCCA  ATGCTACTCA  281  CAATCTCCTA  CAATCTCCTA  A	AACAAACAGC  TATCAATCCG  TATCAATCCG  291  CAACAAAAAT TGTCGCAACC TGTCGCAACC TGTCGCAACC TGCGCTCCAA  TGCCTAACCA TGCCTAACCA TGGCCGACTT
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 82 SEQ 84 SEQ 1 SEQ 2 SEQ 1 SEQ 2 SEQ 2 SEQ 2 SEQ 2 SEQ 23 SEQ 25 SEQ 26	201 TCTGTGCCTG TCTGTGCCTG TCTGTGCCTG	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG CTTGACAACA	CTTGTAGTGA  221  GTATATAAAT GTATATAAAT	231 AAAGATCACC AAAGATCACC TCCTCGCCGA	Z41  GCACCGAGGA  GCACCGAGGA  CCGATTGCCTC	ATAAATACCT  251  GITTCTTACC GITTCTTACC TACCCCCGCA	ATACTIGTTT  261  AACCCATCAA AACCCATCAA TAGTCACACT	CGCACGTCCG	ATGCTACTCA  ATGCTACTCA  281  CAATCTCCTA  A ATGACAG TTCTCCCACC	AACAAACAGC  TATCAATCCG  291  CAACAAAAAT TGTCGCAACC TGGGTTCCAA TTCCATACCA TGGCCGACTT
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 1 SEQ 2 SEQ 4 SEQ 1 SEQ 12 SEQ 15 SEQ 12 SEQ 15 SEQ 12 SEQ 20 SEQ 21 SEQ 23 SEQ 26 SEQ 26 SEQ 28 SEQ 29	201 TCTGTGCCTG TCTGTGCCTG TGACCCTCTC TGACCCTCTC	211  GCGCAGACGG GCGCAGACGG CTTGACAACA GTGGTTGAAT	221  GTATATAAAT GTATATAAAT  AAGCCGCCCA TGGTATATTA	231  AAAGATCACC AAAGATCACC TCCTCGCCGA GACCGGAGTA	241  2GCACCGAGGA GCACCGAGGA CCGATTGCCTC CTCTATATGC	251  GITTCTTACC GITTCTACC GITT	ATACTTGTTT  261  AACCCATCAA  ACCCATCAA  ACCCATCAA  ACCCATCAA  ACCCATCAA  ACCCATCAA  ACCCATCAA  ACCCATCAA  ACCCATCAA  ACCCATCAA	271 TAACCATCCA TAACCATCCA TCACCATCCA TCCACCATCCA TCCCACCATCCA TCCCACCATCA TCCCACATCA TCCCACCATCA TCCCACATCA TCCCACCATCA TCCCACCATCA TCCCACCATCA TCCCACCATCA TCCCACCATCA TCCCA	281  CAATCTCCTA CAATCTCCTA	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 82 SEQ 84 SEQ 15 SEQ 1 SEQ 2 SEQ 1 SEQ 2 SEQ 2 SEQ 2 SEQ 2 SEQ 2 SEQ 2 SEQ 23 SEQ 26 SEQ 28 SEQ 29	201 TCTGTGCTG TCTGTGCCTG TCTGTGCCTG TGACCCTCTC	TTGCATGTCA  211  GCGCAGACGG GCGCAGACGG  CTTGACAACA GTGGTTGAAT	221  GTATATAAAT GTATATAAAT GTATATAAAT AAGCCGGCCA TGGTATATTA	231  AAAGATCACC AAAGATCACC TCCTCGCCGA GACCGGGGTA	TGTAAATTTT  241  2CACCGAGGA GCACCGAGGA CCGATTGCCTC CTCTATATGC	251 251 CHITCHTACC GITTCTTACC GITTCTTACC GTTCTTACC GTTCTTACC GAGAGACTAT	ATACTTGTTT  261  AACCCATCAA AACCCATCAA TAGTCACACT	CGCACGTCCG	CCTCGACCCA ATGCTACTCA  281  CAATCTCCTA AATCTCCTA AATCTCCTA TATGACAG ATCTCCTA TTCTCCCACC	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 1 SEQ 2 SEQ 4 SEQ 1 SEQ 12 SEQ 15 SEQ 12 SEQ 15 SEQ 12 SEQ 20 SEQ 21 SEQ 23 SEQ 26 SEQ 26 SEQ 28 SEQ 29	201 TCTGTGCCTG TCTGTGCCTG TCTGTGCCTG TGACCCTCTC TGCTGTAGAT	211  GCGCAGACGG GCGCAGACGG CTTGACAACA GTGGTTGAAT	221  GTATATAAAT GTATATAAAT  AAGCCGCCCA TGGTATATTA	231  AAAGATCACC AAAGATCACC TCCTCGCCGA GACCGGAGTA GTCAAGACCT	241  GCACCGAGGA GCACCGAGGA CCGATTGCCTC CTCTATATGC	ATAAATACCT  251  GTTTCTTACC GTTTCTTACC GTTCTTACC GTTCTTA	ATACTTGTTT  261  AACCCATCAA AACCCATCAA TAGTCACACT ACATTGAAGT GCAATATGGC	271 TAACCATCCA TAACCATCCA TGCCAACGTTC TGCCAACGTT	CCTCAGGTTC  CAATCTCCTA  CAATCTCCTA  CAATCTCCTA  CAATCTCCCAC  CTTCCCAGGTT  CCTAAGGTGTG  CCTAAGGTGTG  CCTAAGGTGTG  CCTTAAGGTGTG  CCTTAAGGTGTG  CCTTAAGGTGTG  CCTTAAGGTGTG  CCTTAAGGTGTG  CCTTAAGTGTG	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 31 SEQ 37 SEQ 37 SEQ 41 SEQ 43 SEQ 82 SEQ 84  SEQ 17 SEQ 2 SEQ 4 SEQ 1 SEQ 2 SEQ 3 SEQ 2 SEQ 3 SEQ 2 SEQ 3 SEQ 2 SEQ 3	201 TCTGTGCCTG TCTGTGCCTG TCTGTGCCTG TGACCCTCTC TGGCGTGAGAT AGAAGATCAA	211 211 2CCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	221  GTATATAAAT GTATATAAAT GTATATAAAT  AAGCCGGCCA TGGTATATATA ATACACACTT	231  AAAGATCACC AAAGATCACC ACCCCCGAGGGATA GACCGGAGTA GTCAAGACCT	241  241  GCACCGAGGA GCACCGAGGA CCGATTGCCTC CTCTATATGC	251  GITTCITACC GAGAGACTAT TCAAAAATCA	ATACTTGTTT  261  AACCCATCAA AACCCATCAA TAGTCACACT ACATTGAAGT ACATTGAAGT	271 TAACCATCCA TAACCATCCA TACCATCCA TACCATCA TACCATCCA TACCATCA TACCATCCA TACCATCA TACCATCCA TACCATCCA TACCATCCA TACCATCCA TACCATCCA TACCATCA TACCATCCA TACCATCA	CCTCGACCCA ATGCTACTCA ATGCTACTCA CAATCTCCTA AAATCTCCTA AAATCTCCTA AAATCTCCTA TTCTCCCACC CTTCCACACT CCTAAGTGTG	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 15 SEQ 11 SEQ 13 SEQ 15 SEQ 11 SEQ 13 SEQ 12 SEQ 15 SEQ 21 SEQ 22 SEQ 26 SEQ 26 SEQ 27 SEQ 27 SEQ 21 SEQ 23 SEQ 26 SEQ 27 SEQ 27 SEQ 28 SEQ 28 SEQ 29 SEQ 21 SEQ 23 SEQ 26 SEQ 27 SEQ 28 SEQ 29 SEQ 21 SEQ 23 SEQ 26 SEQ 27 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37	201 TCTGTGCCTG TCTGTGCCTG TCTGTGCCTG TGACCCTCTC TGACCCTCTC TGACCCTCTC	211  GCGCAGACGG GCGCAGACGG CTTGACAACA GTGGTTGAAT ACAGTCCCCT	CTTGTAGTGA  221  GTATATAAAT  GTATATAAAT  AAGCCGGCCA  TGGTATATTA  ATACACACTT	231  AAAGATCACC AAAGATCACC AAAGATCACC AGAGACCAC  TCCTCGCCGA GACCGGAGTA  GTCAAGACCT	241  GCACCGAGGA GCACCGAGGA CCGATTGCCTC CTCTATATGC ATCTATTATT	251  GITTCTTACC GITTCTACC GITTCTTACC GITTCTA	ATACTTGTTT  261  AACCCATCAA  AACCCATCAA  TAGTCACACT  ACATTGAAGT  GCAATATGGC	271 TAACCATCCA TGCCAACGTT	CCTAAGTGTG	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 34 SEQ 36 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 15 SEQ 1 SEQ 1 SEQ 1 SEQ 1 SEQ 1 SEQ 2 SEQ 1 SEQ 2 SEQ 1 SEQ 2 SEQ 2 SEQ 3	201 TCTGTGCCTG TCTGTGCCTG TCTGTGCCTG TGACCCTCTC TGACCCTCTC	211 211 2CGCAGACGG GCGCAGACGG CTTGACAACA CTTGACAACA ACAGTCCCCT	221  GTATATAAAT GTATATAAAT GTATATAAAT  AAGCCGGCCA TGGTATATATA ATACACACTT	231  AAAGATCACC AAAGATCACC TCCTCGCCGA GACCGGAGTA GTCAAGACCT	Z41  GCACCGAGGA  GCACCGAGGA  CGATTGCCTC  CTCTATATGC  ATCTATTATT	251  GITTCTTACC GITTCTTACC GITTCTTACC GITTCTTACC GITTCTTACC TACCCCCGCA GAGAGACTAT TCAAAAATCA	ATACTIGITT  261  AACCCATCAA AACCCATCAA TAGTCACACT ACATTGAAGT	271 TAACCATCCA TAACCATCCA TCGCACGTCCG TGCCAACGTT TGAGGACAATG	CCTCGACCCA  ATGCTACTCA  ATGCTACTCA  CAATCTCCTA  AAATCTCCTA  AAATCTCCTA  AAATCTCCTA  TTCTCCCACC  CTTCCCAGATT  CCTAAGTGTG	AACAAACAGCGAAC
SEQ 25 SEQ 26 SEQ 28 SEQ 29 SEQ 32 SEQ 37 SEQ 39 SEQ 41 SEQ 43 SEQ 82 SEQ 84 SEQ 15 SEQ 11 SEQ 13 SEQ 15 SEQ 11 SEQ 13 SEQ 12 SEQ 15 SEQ 21 SEQ 22 SEQ 26 SEQ 26 SEQ 27 SEQ 27 SEQ 21 SEQ 23 SEQ 26 SEQ 27 SEQ 27 SEQ 28 SEQ 28 SEQ 29 SEQ 21 SEQ 23 SEQ 26 SEQ 27 SEQ 28 SEQ 29 SEQ 21 SEQ 23 SEQ 26 SEQ 27 SEQ 28 SEQ 29 SEQ 32 SEQ 34 SEQ 36 SEQ 37	201 TCTGTGCCTG TCTGTGCCTG TCTGTGCCTG TGACCCTCTC TGACCCTCTC TGCTGTAGAT	211  211  CTTGCATGTCA  CTTGCATGTCA  GCGCAGACGG  CCTTGACAACA  GTGGTTGAAT  ACAGTCCCCT	221  GTATATAAAT GTATATAAAT GTATATAAAT  AAGCCGGCCA TGGTATATTA	231  AAAGATCACC AAAGATCACC AAAGATCACC GACCGGAGTA GTCAAGACCT TTCAATCACACA	241  241  GCACCGAGGA GCACCGAGGA CTCTATATGC ATCTATATTT	251  GITTCTTACC GITTCTTACC GITTCTTACC GITTCTTACC GITTCTTACC GITTCTTACC GITTCTTACC GITTCTTACC CAGGCTATT TCAAAAATCA CAGGCTATTC	ATACTTGTTT  261  AACCCATCAA ACCCATCAA ACCCATCAA ACCTTGAAGT  TAGTCACACT ACATTGAAGT GCAATATGGC CCGTCCTTTC	CGAAA  CTTCACTTCT  TAACCATCCA  TAACCATCCA  CGCACGTCCG  TGCCAACGTT  TGAGACAATG  TTCCCAGAAT	CCTTCCCCACC CTTCCCAGATT CCTAAGTGTG	AACAAACAGCGAAC

SEC			311	321	331	341			371		391
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	1	GACTGTCGCC	GATATCGACG	TTCCTCCTGC	CGAGGGCATC	CCCTACTTCA	CTCCGGCCCA	GAACCCTCCT	GCCGGTACGG	CAGCTAACCC	CCAGACCAAT
	2						CTCCGGCCCA				
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	28						CACCGGCTCA				
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	34						CTCCAGTGCA				
	36						CGCCTGCTCA				
	37						CGCCTGCTCA				
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	43						CCCCACCACG				
	82						ACCCTGAGCA				
SEC	84	ACCGCCTCTC	GTCGACTCGA	TCGATGCACT	CAAGATCAGC	AACTTIGICC	CCACTCGAAG	IGGCCACCCI	CCICCIGGCI	CGGTCCCGGA	ATCCATCCTG
			411			441			471	481	491
SEC	1						CGTCACC				
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SEC		GGAT	CGGCACCTCC	CAAGCTCTTC	CGGCCGCTTT	CGGTGCGGGG	TCTGACC			-TTTCACAAT	CGCATTGGCG
SEC		GGAI	GACCCC	TACGCTCTTC	CGGCCCTTAC	AAATCCGCAA	TGTGACG			-CTCAAGAAC	CGCATCATG-
SEC		GGCA	ATGCCGTCCC	CAAGCTGTAC	ACACCTCTGA	CGGTGCGTGG	GGTGACC			-TTCCACAAC	AGACTTGGC-
	11						GCTTGCT CTCGATC				
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SEQ	17			-AAACTCTCC	CAACCCCTCA	CCCTCCCCAA	TGGCCTT		AC	CCTCCCCAAC	CGCCTCGTC -
	18			-AAACTCTCC	CAACCCCTCA	CCCTCCCCAA	TGGCCTT		AC	CCTCCCCAAC	CGCCTCGTC-
	20						CGTCGAG				
	23						AGTGGAG				
	25						CCTCACC				
	26 28						CCTCACC				
	29						CGTCACA				
	32										
SEQ	34	GG		AAGCCTATTC	TCTCTTATTA					-CTTCAAAAC	
SEQ SEQ		GG		AAGCCTATTC AGGTTTTC	TCTCTTATTA ACACBCATCA	CCATCCGAGG	CGTCACA CGTCACA			-CTTCAAAAC -TTCCCAAAC	CGTCTCTTT-
SEQ SEQ SEQ	34 36 37 39	GG		AAGCCTATTC AGGTTTTC AGGTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCA CCTCA	CCATCCGAGG CCATCCGAGG AGATCCGAGG	CGTCACA CGTCACA TCTTACC			-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC	CGTCTCTTT- CGTCTCTTT- CGTATTATG-
SEQ SEQ SEQ SEQ	34 36 37 39 41	GG		AAGCCTATTCAGGTTTTCAGGTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCA CCTCA	CCATCCGAGG CCATCCGAGG AGATCCGAGG	CGTCACA CGTCACA TCTTACC			-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC	CGTCTCTTT- CGTCTCTTT- CGTATTATG-
SEQ SEQ SEQ SEQ SEQ	34 36 37 39	GG	ACGC	AAGCCTATTCAGGTTTTCAGGTTTTCCGCTCAAATA	TCTCTTATTA ACACBCATCA ACACBCATCACCTCACCTCA CCCCGTCTCG	CCATCCGAGG CCATCCGAGG AGATCCGAGG 	CGTCACA CGTCACA TCTTACC			-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -CTCCAGAAC	CGTCTCTTT- CGTCTCTTT- CGTATTATG- CGGTTCCTC-
SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 39 41 43	GG	ACGC	AAGCCTATTCAGGTTTTCAGGTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCACCTCACCCCGTCTCG ACACCCATCA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG- AGATTCGCGG	CGTCACA CGTCACA TCTTACC			-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC	CGTCTCTTT- CGTCTCTTT- CGTATTATG- CGGTTCCTC- CGTATCTGG-
SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 39 41 43	GGA CCAGAGGGTG	ACGC ATACTCTACC TCAAAAAACC	AAGCCTATTCAGGTTTTCAGGTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCACCTCACCTCA CCCCGTCTCG ACACCCATCA CAAACGTTGA 531	CCATCCGAGG CCATCCGAGG AGATCCGAGG 	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG	GAACAGGCGG	GTAAGATGAC	-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -CTCCAGAAC -ATGCCCAAC -ATGCCCAAC CTTCAAGAAC	CGTCTCTTT- CGTATTATG- CGGTTCCTC- CGTATCTGG- CGCATCATT-
SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 39 41 43	GGA CCAGAGGGTG	ACGC ATACTCTACC TCAAAAAACC	AAGCCTATTCAGGTTTTCAGGTTTTCCGCTCAAATA AAAGGTCTTT GGCTTTGTTC	TCTCTTATTA ACACBCATCA ACACBCATCACCTCA CCCCGTCTCG ACACCCATCA CAAACGTTGA 531	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG- AGATTCGCGG CATTGCCCTT	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG	GAACAGGCGG	GTAAGATGAC	-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC	CGTCTCTTT- CGTATTATG- CGGTTCCTC- CGTATCTGG- CGCATCATT-
SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 39 41 43 82 84	GGA CCAGAGGGTG 501 TAAGTCCGTT	ACGC ATACTCTACC TCAAAAAACC	AAGCCTATTC - AGGTTTTC - AGGTTTTC - CGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCACCTCA CCCCGTCTCG ACACCCATCA CAAACGTTGA 531	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGG CATTGCCCTT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG	GAACAGGCGG	GTAAGATGAC	-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC	CGTCTCTT- CGTATTATG- CGTATTATG- CGTATCTCC- CGTATCTGG- CGCATCATT- 591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 39 41 43 82 84	GGA CCAGAGGGTG 501 TAAGTCCGTT	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT	AAGCCTATTCAGGTTITTCAGGTTITTCAGGTTITTC	TCTCTTATTA ACACBCATCA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAAACGTTGA 531 AAAGCTAATC	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCCGT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG	GAACAGGCGG 561	GTAAGATGAC	-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC 581CTCGC	CGTCTCTTT- CGTCTTTTT- CGTATTATG- CGTATCTGG- CGCATCATT- 591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 39 41 43 82 84	GGA CCAGAGGGTG 501 TAAGTCCGTT TGAGTGCAGT	ACGC ATACTCTACC TCAAAAAACC 511	AAGCCTATTCAGGTTTTCAGGTTTTCGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCGTTGA 531 AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGG CATTGCCCTT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG 551 TGGAACAGCC	GAACAGGCGG 561	GTAAGATGAC 571	-CTTCAAAAC -TTTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC 581	CGTCTTT- CGTATTATG- CGTATCTG- CGGTATCTG- CGCATCATT-  591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 39 441 43 82 84 84	GGA CCAGAGGGTG 501 TAAGTCCGTT TGAGTGCAGT	ACGC ATACTCTACC TCAAAAAACC 511	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCCGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA ACACCCATCA CCCCGTCTCG ACACCCATCA CAPACGTTGA 531 AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGG CATTGCCCTT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG	GAACAGGCGG 561 GCTTACAGGG	GTAAGATGAC 571 	-CTTCARANC -TTCCCANC -TTCCCANC -CTCCAGAC -CTCCAGAC -GCGCCCANC -ATGCCCANC CTTCANGANC 581	CGTCTCTTT- CGTCTCTTT- CGTATTATG- CGTATCTGG- CGCATCATT-  591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 39 441 443 82 84 84	GGA CCAGAGGGTG 501 TAAGTCCGTT TGAGTGCAGT	ACGC ATACTCTACC TCAAAAAACC 511	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTC CGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCGTTGA 531 AAAGCTAATC TCCTATGCGA	CCATCCAGG CCATCCAGG AGATCCAGG GGGCGCTCG AGATTCCCCT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 GCTTACAGGG	GTAAGATGAC 571 	-CTTCAAAAC -TTTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC 581	GGTCTCTTT- CGTATTATG- CGTATCTGG- CGGATCATT-  591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 37 39 41 41 43 82 84 82 84	GGA CCAGAGGGTG 501 TAAGTCCGTT TGAGTGCAGT	ACGC ATACTCTACC TCAAAAAACC 511	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTC CGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCCATCA CAAACGTTGA S31 AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGG CATTGCCCTT 541	CGTCACA CGTCACA CTTTACC CATGACC TGCTGCACCG 551 TGGAACAGCC	GAACAGGCGG 561 GCTTACAGGG	GTAAGATGAC 571 	-CTTCARANC -TTCCCANAC -TTCCCAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC  581	CGTCTCTTT- CGTCTCTTT- CGTATTATG- CGTATCTGG- CGCATCATT-  591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 37 39 41 43 48 84 84 84 1 2 2 4 3 7 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GG		AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCCGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCGTTGA 531 AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 	GTAAGATGAC 571 	-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC 581	GGTCCTTT- CGTCTCTTT- CGTATTATG- CGTATCTGG- CGCATCATT-  591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 36 37 37 39 41 43 43 43 43 44 43 44 45 77 99 11 13	GGA CCAGAGGGTG 501 TAAGTCCGTT TGAGTGCAGT	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCCGCTCAAATA AAAGGTCTTT 521CATATCGACG ATGCTATCCA	TCTCTTATTA ACACBCATCA ACACBCATCA ACACCCATCA CCCCGTCTCG ACACCCATCA CAAACGTTGA 531 AAAGCTAATC TCCTATGCGA	CCATCCAGG CCATCCAGG AGATCCCAGG GGGCGGTCG AGATTCCCCG CATTGCCCTT 541	CGTCACA CGTCACA CTTTACC CATGACC TGCTGCACCG 551 TGGAACAGCC	GAACAGGCGG 561 GCTTACAGGG	GTAAGATGAC 571 AATGATAATG	-CTTCARANC -TTCCCANC -TTCCCAAC -CTCCAGAAC -CTCCAGAAC -CTCCAGAAC -ATGCCCAAC -ATGCCCAAC -TCGC	GGTCTCTTT- CGTCTCTTT- CGTATTATG- CGGTATCTGG- CGCATCATT-  591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	346 337 337 337 341 443 882 884 884 815 111 113 115 117	GGA CCAGAGGGTG 501 TAAGTCCGTT TGAGTGCAGT		AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCCGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACGTTGA S31 AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGG CATTGCCCTT 541	CGTCACA CGTCACA TCTTACC TGCTGCACCG  S51 TGGAACAGCC	GAACAGGCGG 561 	GTAAGATGAC 571 	-CTTCAAAAC -TTTCCCAAAC -TTTCCCAAAC -CTCCAGAAC -GGGCCCAAC -ATGCCCAAC CTTCAAGAAC  581	GGTCCTTT- CGTATTATG- GGTTCCTC- CGTATCTGG- CGCATCATT-  591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 37 37 37 37 34 44 43 88 82 84 85 7 9 11 13 15 17 17 18 20	GG		AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTCTTT GGCTTATTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAAACGTTGA 531 AAAGCTAATC TCCTATGCGA	CCATCCAGG CCATCCAGG CCATCCAGG GGGCGGTCG AGATTCCCGG CATTGCCCTT 541	CGTCACA CGTCACA CGTCACA CTTACC CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 GCTTACAGGG	GTAAGATGAC 571 	-CTTCARANC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC  581	CGTCTTTTCGTTTTTCGTATTATG- CGTATCTGG- CGGATCATT-  591
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	34 337 337 337 341 443 842 84 84 15 7 9 11 11 11 11 11 11 11 11 11 11 11 11 1	GGA CCAGAGGGTG 501 TAAGTCCGTT TGAGTGCAGT		AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCCGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA ACACCCATCA CCCCGTCTCG ACACCCATCA CANACGTTGA  531 AAAGCTAATC TCCTATGCGA	CCATCCAGG CCATCCAGG AGATCCCAGG GGGCGGTCG AGATTCCCCT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 	GTAAGATGAC 571 	-CTTCARANC -TTCCCANC -TTCCCAAC -CTCCAGAAC -CTCCAGAAC -CTCCAGAAC -ATGCCCAAC -ATGCCCAAC -TCGC	GGTCTCTTT- CGTATTATG- GGTTCCTC- CGTATCTGG- CGCATCATG- 591
SEQ	34 4 3 3 7 9 3 8 8 2 8 4 4 1 1 2 2 4 4 5 5 7 7 9 1 1 1 3 1 5 1 1 7 1 8 8 2 2 5 2 5 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 2 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 2 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 2 5 5 2 7 9 2 5 2 7 9 2 7 9 2 7 9 2 7 9 2 7 9 2 7 9 2 7 9 2 7 9 2 7 9 2 7 9 7 9	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCCATCA CAAACGTTGA AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGG CATTGCCCTT 541 CCCCCGTCAG GCCCTTGCAT	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 	GTAAGATGAC 571 	-CTTCARANC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC  581	GGTCCTTT- CGTATTATG- GGTATCTG- CGTATCTG- CGTATCTG- CGTATCTG- CGCATCATT-  591
SEQ	346 337 337 337 341 443 882 884 84 15 7 9 11 11 13 15 17 18 20 11 11 11 11 11 11 11 11 11 11 11 11 11	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCCGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCGTTGA AAAGCTAATC TCCTATGCGA TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG AGATTCGCGG CATTGCCCTT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 	GTAAGATGAC 571 	-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -ATGCCCAAC -ATGCCCAAC -TTCAAGAAC -CTCAGC	GGTCCTTT- CGTCTCTTT- CGTATTATG- GGTTCCTC- CGTATCTGG- CGCATCATT-  591
SEQ	34 34 37 37 37 37 31 31 31 31 31 31 31 31 31 31 31 31 31	GG		AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTCTTT GGCTCAAATA AAAGGTCTTT 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAAACGTTGA  531 AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCCTT 541	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 GCTTACAGGG	GTAAGATGAC 571 AATGATAATG	-CTTCARANC -TTTCCCANC -TTTCCCANC -CTTCAGANC -CTCCAGANC -CTCCAGANC -CTTCAGANC -CTTCAGANC -CTTCAGANC -CTTCAGANC -CTCGC -CTCGC -CTGGC -CTGGC -GTATC -GTGTC -GTTTC -GTTTC -AAAGC -AAAGC -GTCTC -GTCTCC	GGTCTCTTT- CGTATTATG- GGTATCTGG- CGGTATCTGG- CGCATCATG- 591
SEQ	3 3 4 4 3 3 7 9 3 8 4 4 1 1 3 1 5 7 9 9 1 1 1 3 1 1 5 7 1 7 1 8 1 2 2 1 2 2 3 2 5 6 2 8 2 9 3 2 2 5 6 2 8 2 9 3 2	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCCGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCGTTGA AAAGCTAATC TCCTATGCGA	CCATCCAGG CCATCCGAGG AGATCCGAGG AGATTCGCGG CATTGCCCTT 541	CGTCACA CGTCACA TCTTACC TGCTGCACCG  551  TGGAACAGCC	GAACAGGCGG 561 	GTAAGATGAC 571 	-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GGGCCCAAC -ATGCCCAAC -TTCAAGAAC  581	GGTCCTTT- CGTCTCTTT- CGTATTATG- CGTATCTGG- CGCATCATT-  591
SEQ	346 337 337 337 3441 343 382 382 384 384 384 384 384 384 384 384 384 384	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCCATCA CAAACGTTGA AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGG CATTGCCCTT 541  CCCCCGTCAG GCCCTTGCAT	CGTCACA CGTCACA TCTTACC CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 GCTTACAGGG	GTAAGATGAC 571	-CTTCARANC -TTCCCANAC -TTCCCANAC -CTCCAGAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC  581	GGTCCTTT- CGTATTATG- CGTATTATG- CGGTATCTGG- CGCATCATT-  591  CCCATCTGC GCCACTCTGC GCCACTCTGC GCCACTCTGC GCCACTTGC GCCATGTGC GCCATGTGC GCCATGTGC GCCATGTGC GCCATGTGC GCCATGTGC GCCATGTGC CCCATGTGC CCCCATGTGC CCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTC CCCCATGC CCCCCTC CCCCATGTC CCCCCT CCCCATGTC CCCCCTC CCCCTC CCCCTC CCCCC
SEQ	346 337 337 337 341 341 343 382 382 384 382 384 385 385 385 385 385 385 385 385 385 385	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCCATCA CAAACGTTGA TCCTATGCGA TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGT 541	CGTCACA CGTCACA TCTTACC TGCTGCACCG  551  TGGAACAGCC	GAACAGGCGG 561	GTAAGATGAC 571	-CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC  581	GGTCCTTT- CGTATTATG- GGTATCTGG- CGCATCATT-  591
SEQ	346 337 337 337 344 344 344 344 344 344 345 347 347 347 347 347 347 347 347 347 347	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTC CGCTCAAATA AAAGGTCTTT GGCTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCCATCA CAAACGTTGA AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCCGT 541	CGTCACA CGTCACA CGTCACA CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561  GCTTACAGGG	GTAAGATGAC 571	-CTTCARANC -TTCCCANAC -TTCCCANAC -TTCCCAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC CTTCAAGAAC  581	GGTCTTTT- CGTATTATG- GGTATCTGC- GGTATCTGC- GGTATCTGC- GGTATCTGC- GGTATCTGC- GCCATCTGC GCCACTCTGC GCCACTCTGC GCCATGTGC CCCATGTGC CCCATGTGC CCCATGTGC CCCATGTGC CCCCATGTGC CCCATGTGC CCCCATGTGC CCCATGTGC CCCCATGTGC CCCATGTGC CCCCATGTGC CCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCCATGTGC CCCATGTGC CCCCATGTGC CCCATGTGC CCCAT
SEQ	3 3 4 4 1 3 3 7 9 1 1 3 1 5 7 7 9 1 1 1 3 1 5 7 1 7 1 8 2 2 1 2 2 3 2 4 2 9 3 2 4 3 3 4 6 3 3 7 3 3 9 4 1	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCGATCA CAACCGATCA TCCTATGCA AAAGCTAATC TCCTATGCGA	CCATCCAGG CCATCCGAGG AGATCCGAGG AGATTCGCGG CATTGCCCTT 541	CGTCACA CGTCACA TCTTACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 	GTAAGATGAC 571	CTTCAAAAC -TTCCCAAAC -TTCCCAAAC -TTCCCAAAC -CTCCAGAAC -ATGCCCAAC -ATGCCCAAC -ATGCCCAAC -TTCAAGAAC -CTCGC -CTCGC -CTCGC -CTATC -CTATC -CTATC -GTTGC -GTATC -AAAGC -AAAGC -AAAGC -GTCTC -GTTCA -GTTCA -GTTCA -GTTCA -TTCAG	GGTCTCTTT- CGTCTCTTT- CGTTTTATG
SEQ	346 337 337 337 341 341 342 344 345 379 311 325 327 327 328 329 331 337 337 337 337 337 337 337	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTGTTC 521	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCGTTGA S31 AAAGCTAATC TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG GGGCGGTCG AGATTCGCGG CATTGCCCTT 541  CCCCCGTCAG GCCCTTGCAT	CGTCACA CGTCACA CGTCACA CATGACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561 	GTAAGATGAC 571	-CTTCARANC -TTTCCCANAC -TTTCCCANAC -TTCCCARAC -CTCCAGAAC -CTCCAGAAC -GCGCCCAAC -ATGCCCAAC -TTGCCAAC -TTGCC -CTCGC -CTCGC -CTCGC -CTTGC	GGTCTTTT- CGTATTATG- CGTATTATG- CGGTATCTGG- CGCATCATT-  591
SEQ	346 337 337 337 341 443 882 884 84 122 445 57 991 113 115 115 120 221 225 226 229 324 336 337 411 433 441 443 443 443 443 444 443 444 444	GG	ACGC ATACTCTACC TCAAAAAACC 511 TGCCCTTGCT CCAGGCAATT	AAGCCTATTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTCAGGTTTTC	TCTCTTATTA ACACBCATCA ACACBCATCA CCCCGTCTCG ACACCCATCA CAACCCATCA CAAACGTTGA TCCTATGCGA TCCTATGCGA TCCTATGCGA	CCATCCGAGG CCATCCGAGG AGATCCGAGG AGATCCGAGG AGATTCGCGG CATTGCCTT 541	CGTCACA CGTCACA TCTTACC TGCTGCACCG  551 TGGAACAGCC	GAACAGGCGG 561  GCTTACAGGG	GTAAGATGAC 571	-CTTCARANC -TTCCCANAC -TTCCCANAC -TTCCCAAC -TTCCCAAC -TTCCCAAC -TTCCCAAC -TTCAAGAAC  581	GGTCTCTTT- CGTATTATG- GGTATCTGG- CGGTATCTGG- CGCATCATT-  591

	601	611	621	631	641	651	661		681	691
							******			
SEQ 1							TACCACATCG			
SEQ 2							TACCACATCG			
SEQ 4							TGGCATATGG			
SEQ 5							TGGCATATGG			
SEQ 7							TACCACCTGG TACCACATCG			
SEQ 9 SEO 11							TACCACATEG			
SEQ 13							TTTCATTTTG			
SEQ 15	ACCTACTCTG	CC		GACGATG	GCCACATGAC	CGAC	TGGCACCTTG	TCCACCTGGG	CTCCTTCGCC	CTCCGCGGTG
SEQ 17							CCCGAACTCG			
SEQ 18							CCCGAACTCG			
SEQ 20 SEQ 21							TTCCACTTGG			
SEQ 23							TTTCACCTAG			
SEQ 25							TACCACCTCG			
SEQ 26	CAGTACTCCG	CC		GACAATG	GCCACGCGAC	CGAC	TACCACCTCG	TCCACCTGGG	CCAGTTCGCC	CTGCACGGCG
SEQ 28	· CAATACTCCG									
SEQ 29 SEQ 32							TGGCACTTGA			
SEQ 32							TGGCACAAAC			
SEQ 36							TGGCACTTGA			
SEQ 37							TGGCACTTGA			
SEQ 39							TGGCATCACA			
SEQ 41 SEQ 43							CAGCTGGTGC			
SEQ 82							TGGCACTTTG			
SEQ 84							TACCACATTG			
									202	701
	701	711	721	731	741	751	761	771	781	791
							****			
SEQ 1	CCGGCCTGAT	GCTGATTGAG	GCGACCGCCG	TCCAGCCCGA	AGGCCGC	ATCACCCCTC	AGGATGTCGG	TCTGTGGAAG	GACTCC	CA
SEQ 2							AGGATGTCGG			
SEQ 4							AGGACCTGGG			
SEQ 5 SEQ 7							AGGACCTGGG ACGACTCGGG			
SEO 9							AGGACGTCGG			
SEQ 11							ATGATTTAGG			
SEQ 13							ATGATTTAGG			
SEQ 15							AGTGCTCTGG			
SEQ 17 SEO 18							ACGACATCAG ACGACATCAG			
SEQ 18 SEO 20							AGGACATCAG			
SEQ 21							AGGACAGCGG			
SEQ 23							ATGATTCAGG			
SEQ 25							AGGATGTCGG			
SEQ 26							AGGATGTCGG			
SEQ 28 SEQ 29							AGGATGTTGG AGGATGTTGG			
SEQ 32										
SEQ 34							AGGATGCAGG			
SEQ 36							AGGACGTTGG			
SEQ 37							AGGACGTTGG			
SEQ 39 SEQ 41							AAGACGTCGG			
SEQ 43							ACATGGTGGT			
SEQ 82	CTGGCCTCAT	CATGCTAGAA	GCTACCGCAG	TTCAAGCACG	TGGCCGT	ATCACACCTG	AAGATTCTGG	CATCTGGCTA	GACTCT	CA
SEQ 84	TGGGAAACGT	CATGGTCGAA	GCATCTGGTG	TTGAGCCAGA	GGGGAGG	ATCACGCCTC	AGGACCTGGG	TATTTGGTCG	GAACAG	CA
	801	811	821	831	841	851	861	871	881	891
					5					6
SEQ 1							GCGTG			
SEQ 2 SEQ 4							GCGTG			
SEQ 5							GCGTG			
SEQ 7	ATTCCTGGGG	CTGAAGC	GGGTCGTCGA	GTTCATGCAC	GCACAGGGC-	GCCAAGGTCG	GGATC	CAGCTT	GCGCATGCGG	GCCGGAAAGC
SEQ 9	GATTGCGCCC	ATGAAGC	GCGTCATCGA	CTTCGTGCAC	TCGCAGTCC-	CAGAAGATTG	GCGTG	CAGATT	GCCCACGCCG	GCCGCAAGGC
SEQ 11	AGCAGAGAAA	TTGAAAC	CAATTGTCGA	TTACGCTCAT	TCTCAAAAG-	CAATTAATTG	CCATC	CAATTG	GGCCATGGTG	GTAGAAAAGC
SEQ 13							GTATA			
SEQ 15 SEQ 17							GTATC CGCCTGTGGT			
SEQ 17							CGCCTGTGGT			
SEQ 20	GATCGCTCCT	CTGCGCC	GCATCGTCGA	CTACGTGCAC	AGCCAGGGC-	CAAAAGATCG	CCATC	CAACTG	GCTCATGCCG	GCCGCAAGGC
SEQ 21							CCATC			
SEQ 23	AATGAAGCCG	TTACGAA	GAATTGTTGA	ATTTGCTCAT	TCGCAAAAT-	CAAAAAATTG	GGATT	CAATTG	GCGCATGCTG	GTAGAAAGGC
SEQ 25 SEQ 26	GATTGCGCCG	CTGAAGC	GCATCGTCGA	CTTTATCCAC	TCGCAGAAC-	CAGGTCGCGG	CCATC	CAGCTC	GCCCACGCCG	GTCGCAAGGC
SEQ 28							GTATC			
SEQ 29	GATCGAGCCT	CTGAAGC	GCATCACCAC	TTTCGCGCAC	AGTCAGAGC -	CAGAAAATTG	GTATC	CAGCTG	TCGCATGCGG	GTCGCAAGGC
SEQ 32							~~~~~			
SEQ 34 SEQ 36							CTATT GTAT			
SEQ 36 SEQ 37	AATCGAGCCC									
SEQ 39	GATCGAGCCT	CTTGCCAA	GGTCGTC-GA	GTTTGCCCAC	TCCCAGAAC-	CAGAAGATCA	TGATT	CAGTTG	GCGCATGCGG	GCCGCAAAGC
SEQ 41										
SEQ 43 SEQ 82							GCG			
SEQ 82 SEQ 84							GTGTA			

	901	911	921	931	941	951	961	971	981	991
SEQ 1										CGGATGGCCG
SEQ 2										
SEQ 4										
SEQ 5	CAGCACCGTC	GCGCCATGGC	TCTCG				-GCCAACGAT	ACCGCCTCCG	AGAAGATGGG	CGGCTGGCCA
SEQ 7						AGGCGGGCAA				
SEQ 9						AA				
SEQ 11										
SEQ 13										
SEQ 15						CAGCGCGG				
SEQ 17						GGGAGAAGGC				
SEQ 18						GGGAGAAGGC				
SEQ 20 SEQ 21						AGCCGAGAGA AGCCGAGAGA				
SEQ 23						AGCCGAGAGA				
SEQ 25						GAGGCTCG				
SEO 26						GAGGCTCG				
SEQ 28	CAGTTGCGTA	TCTCCCTGGC	TAAGC				-GTAAATGCT	GTCGCGGCGG	AAGAAGTGGG	TGGCTGGCCA
SEQ 29										
SEQ 32										
SEQ 34										
SEQ 36										
SEQ 37										
SEQ 39										
SEQ 41						GACT				
SEQ 43	CUGUGGCAGC	GTCCAGCAGC	MCCCC			ATTAGCGC	- CCCCCACGTG	CCCCCCTCAAGC	ACCCCCCCCCC	TCCATCCCC
SEQ 82 SEQ 84						GCGGAGAAAA				
250 04	GAAGGCCTCG	GACTOOTCAC	CITIC		IACC	GCGGMGAGAG	annoconno	TTTOTORCOC	ACCHICC. DICC	
		1011				1051				1091
SEQ 1										
SEQ 1										
SEQ 4										
SEO 5										
SEQ 7						ATATCTTTAG				
SEQ 9										
SEQ 11										
SEQ 13	GAA-CATTGT	GTGGGGCCAT	CTACTGAG				-CCATTTAGT	GATTCACACA	ATACACCACG	AGAATTGACT
SEQ 15	GAG-AACGTC	TGGGCCCCCA	GCGCCATC			AG	CTACAACGAG	GAGACCTTCC	CCTTCCCCAA	GGAGATGACC
SEQ 17										
SEQ 18										
SEQ 20	GAT-GACGTC	TGGGCCCCGA	GCGCCATC				-CCGTTCTCG	GAGGACTTTC	CGAACCCCAA	GGAGATGACC
SEQ 21										
SEQ 23										
SEQ 25	GAC-GACGTT	GTGGCTCCCA	GCGCGATT				-CCTTACACC	AAGGACTGGG	CCACACCGCG	TGAGTTGACT
SEQ 26	GAC-GACGTT	GTGGCTCCCA	GCGCGATT				-CCTTACACC	AAGGACTGGG	CCACACCGCG	CCCTTTCACT
SEQ 28 SEQ 29						GC				
SEQ 32										
SEQ 34										
SEQ 36	GAC-AACATT	GTTGCTCCTT	CTGCCATC			GC	ACAAGAAGCT	GGCGTGAACC	CTGTTCCCAA	GGCCTTCACC
SEQ 37	GAC-AACATT	GTTGCTCCTT	CTGCCATC			GC	ACAAGAAGCT	GGCGTGAACC	CTGTTCCCAA	GGCCTTCACC
SEQ 39	CAG-GATGTC	TGGGCGCCCA	GTGCGATT				-CCATGGAAC	GAGAAGCACG	CTGTCCCAAA	GGAGATGTCG
SEQ 41						GGTCCTCGAG				
SEQ 43							TTTGGG	TCAAAGTTTG	GCGTGCCCAG	GCCCGCTACC
SEQ 82										
SEQ 84	GAT-CGTGTC	GTCGCTCCTT	CGGCCATC				-GCATATGCG	CAAGGTCACG	Traceceres	AGCTCTCACG
		1111		1131					1181	1191
SEQ 1						GCGCCATCGC				
SEQ 2						GCGCCATCGC GGGCTGTTAA				
SEQ 4 SEQ 5						GGGCTGTTAA				
SEQ 7						TAGCGGTGCA				
SEO 9						GGGCCATTGC				
						GAGCTGTTGA				
						GGGCTGTGGA				
SEQ 15	GTCGAGCA-G	ATCCACGAGC	TCGTCGAGGC	CTGGAAGGCG	TCTGCCCAGC	GTGCCCTCAA	GGCCGGC	TTCGACCTCA	TTGAGATCCA	CGCCGCCCAC
SEQ 17	GTTGCGGA-G	ATCAAGGATA	TCGTGCAAAA	GTTTGCGGTG	ACGGCGAGGA	TCACGGCCGA	GGCCGGG	TTCAATGGCG	TGGAGATCCA	TGCGGCGCAT
						TCACGGCCGA				
						GTGCCATCGA				
						GTGCCATCGA				
						GTGCAGTTGA				
SEQ 25	ACCGAGGRRG	TCGAGGGTCT	CCCTCAAGAA	GTTCGCCGAG	TCCCCCAAGA	GGTCAAATCG	AGCIGGT	TITIGACGICA	TIGAGATUCA	CCCCCCTCA-
						GGTCAAATCG GAGCCATCCA				
						GAGCCATCCA				
SEQ 32						GAGCCAICCA				
SEQ 34										
	AAGGAGGA-T	ATCGAGGAAC	TCAAGAATGA	CTTTCTGGCT	GCAGCMAAAC	GAGCCAWCCG	CGCTGGT	TTTGATGTCA	TCGAGATCCA	TGCAGCTCAT
						GAGCCAWCCG				
SEQ 39	TTGGATGA-T	ATCGAGGCTT	TCAAGAAGGC	GTTTGGAGAG	GCGGTCAAGC	GGGCATTGAA	GGCTGGA	TTTGATGTTA	TTGAGATTCA	CAATGCTCAC
						GGGCGGTGAA				
						ACCTIGAAAA				
						GAGCGGTTGA				
SEQ 84	ACCGAGGA-C	ATCAACAAGT	LGCAAGACAA	ATTCGTTCAG	LUGUACGAT	ADI-1-16A	MGC1666	THIGHCIACG	I COMMCTTCA	CAGCGCTCAC

									1281	1001
	1201		1221							
SEO 1			CCTCTCGCCG							
SEQ 2	GGATACCTGC	TGTCGTCATT	CCTCTCGCCG	GCCGCCAAC-						
SEQ 4	GGCTATCTTC	TGATGTCGTT	CCTCTCCCCT	GCGGTCAAC-						
SEQ 5	GGCTATCTTC	TGATGTCGTT	CCTCTCCCCT	GCGGTCAAC-						
SEQ 7	GGCTATCTCA	TCAACGAGTT	CCTGAGCCCG	GTCACGAAT-						
SEQ 9	GGGTATCTTC	TCTCGTCTTT	CCTATCACCG CTATAGTCCT	TCTTCCAAC-						
SEQ 11 SEQ 13	CCATCTTTTGA	TIAATGAGTI	TTTAAGTAAA	TTCACAAAC-						
SEQ 15	GGCTACCTCA	TTTCCGAGTT	CTTGAGCCCC	ATCTCCAAC-						
SEQ 17	GGATACCTGT	TGGCGCAGTT	CTTGAGCAAG	AAGACAAAC-						
SEQ 18	GGATACCTGT	TGGCGCAGTT	CTTGAGCAAG	AAGACAAAC-						
SEQ 20	GGTTACCTGA	TCACCGAGTT	CCTTTCGCCG	CTATCAAACG	TAAGTGGAGA	TACTTTGTGT	GGGGCTGTGC	GCATACTCCC	TCGGGTGTGA	CTTCTATTAA
SEQ 21			CCTTTCGCCG							
SEQ 23			AGTTAGTCCT							
SEQ 25										
SEQ 26 SEO 28			CTTGAGTCCG							
SEQ 28 SEQ 29			CTTGAGTCCG							
SEQ 32			CIIGAGICCG							
SEQ 34										
SEQ 36			CTTGAGTCCA							
SEQ 37	GGATACKTGC	TTCACCAGTT	CTTGAGTCCA	GTCAGTAAC~						
SEQ 39	GGATACCTCC	TCCACGAATT	CATCTGCCTG	AGAGCAACA-						
SEQ 41	GGGTACCTCA	TCCACGAATT	CCTCTCACCC	ATTACCAAC-						
SEQ 43	GGTTACCTGC	TGGCCCAATT	CCTGTCCGAA	ACAACCAAC-						
SEQ 82	GGTTATCTTG	TECACTO	CCTGTCCCCT	GCCACCAAC-						
SEQ 84	GGMIACCIGA	IGCACTCGTT	CCICAGCCCG	I I GACCAA!-						
	1301	1311	1321	1331	1341	1351	1361	1371	1381	1391
SEQ 1			AACCGCAC							
SEQ 2			AACCGCAC							
SEQ 4			ACGAGAAC	AGACGAGTAC	GGAGGCAGTT	TTGAGAATCG	CATCCGGCTC	AGTCTGGAGA	TCGCCAAGCT	CACCCGCGAA
SEQ 5 SEQ 7			ACGAGAAC AAGCGGAC							
SEO 9			ACGCGCAC							
SEO 11			AAGAGAAC							
SEQ 13			AAGAGAGC	TGACCAATAC	GGGGGCTCAT	TTGAAAACAG	AGTTAGATTT	CTTTTACAAA	TAATTGAGAA	TATAAAACGA
SEQ 15			CAGCGTAC	CGACCAGTAC	GGTGGCTCCT	TCGAGAACCG	CACCCGCGTT	CTCCGCGAGA	TCATCTCGGC	CGTCCGCTCC
SEQ 17			AGGCGCGG							
SEQ 18			AGGCGCGG							
SEQ 20			AGAAACGGAC							
SEQ 21			AAACGGAC							
SEQ 23			GACCGCAA							
SEQ 25 SEQ 26										
SEQ 28			CAAAGAAC							
SEO 29			CAAAGAAC	CGACGAGTAT	GG					
SEQ 32			AAC	CGACGAGTAT	GGTGGCAGTT	TCGAGAACCG	TATCAGAGTT	GTCTTGGAAA	TCCTTGACCT	CATCCGCGCT
SEQ 34										
SEQ 36			CAAAGAAC							
SEQ 37			CAAAGAAC							
SEQ 39			CCAGGACC							
SEQ 41 SEO 43			CGCCGGAC CAGCGCAC							
SEQ 43 SEQ 82			AAGCGTAC							
SEQ 84			CAGCGTAC							
	1401	1411	1421	1431	1441	1451	1461	1471	1481	1491
SEQ 1			C							
SEQ 2 SEQ 4			T							
SEQ 5	AATGTGCCCA	AGGATATGCC	T		GTCTT	CCTGCGGGTC	TCCGCCACCG	ATTGGCTGGA	GGAGGTGCAG	CCGAA
SEQ 7			C							
SEQ 9			T							
SEQ 11	AGTATTCCAA	ACGATGTTCC	A		GTGTT	TTTGAGAATC	TCTGCTGCTG	AAAATAGTCC	TGATCCA	
SEQ 13			G							
SEQ 15			C							
SEQ 17			TGAAGAGGAG							
SEQ 18			TGAAGAGGAG							
SEQ 20	CTCATTCCCG	AGGAGATGCC	A		CTCTT	CCTCCGAATC	TCCGCGACCG	AAIGGAIGGA	GTACGCCGGC	
SEQ 21 SEQ 23			C							
SEQ 25										
SEQ 26										
SEQ 28										
SEQ 29										
SEQ 32			T							
SEQ 34										
SEQ 36 SEO 37										
SEQ 37 SEQ 39										
SEQ 41					CTCTT					
SEQ 43			C		CTCGG	CATCAAAATT	AACAGCGTCG	AGTTCCAGGA	GAAG	
SEQ 82	CGGACGAGCA GTTATGCCTG	AGAATTTCAT AGGACATGCC	C		TTGTT	CACTCGCATC	AGTGGAACTG	ACTGGCTGGA	GAACAACCCT	GAG
	CGGACGAGCA GTTATGCCTG	AGAATTTCAT AGGACATGCC	C		TTGTT	CACTCGCATC	AGTGGAACTG	ACTGGCTGGA	GAACAACCCT	GAG

## 10/17

	1501			1531					1581	1591
SEQ 1							AGCAGGGCGC			
SEQ 2		GCAGAGCTGG	AAGTCGGAGG	ATACCGTGCG	GTTCGCGCAG	GAGCTGGTCA	AGCAGGGCGC	CGTTGATCTG	ATCGATATCA	GCAGCGGTGG
SEQ 4							AAACGGGTTA			
SEQ 5 SEQ 7							AAACGGGTTA CCGAATGGGG			
SEQ 7							CCCAGGGCGC			
SEQ 11		-GAAGCTTGG	ACTATTGAAG	ATTCCAAAA-	AATTAGCT	GACATTTTAG	TAGAAAAGGG	TATTGCTTTG	GTTGATGTTT	CATCTGGTGG
SEQ 13							TTGATTTAGG			
SEQ 15							CCGACCTCGG AGCAGTGGGG			
SEQ 17 SEQ 18							AGCAGTGGGG			
SEQ 20	GA	GCCTAGCTGG	GACCTCGAGC	AGAGCACAC-	AGCTTGCC	AAGCTCCTCC	CGGACCTGGG	TGTCGACCTG	CTCGACGTCA	GCTCGGGCGG
SEQ 21							CGGACCTGGG			
SEQ 23 SEO 25							GCGATGGTGG			
SEQ 26										
SEQ 28										
SEQ 29										
SEQ 32 SEQ 34							CCAAGCATGG			
SEQ 34										
SEQ 37										
SEQ 39										
SEQ 41							CCGACTTGGG AGGCCGCGGG			
SEQ 43 SEQ 82							CAGACCGTGG			
SEQ 84							AAGAGGCTCG			
	1601	1611	1621	1631	1641	1651	1661	1671	1681	1691
	#########	######								
SEQ 1 SEQ 2	TGTTCTCGCG	CAG								
SEQ 4	CACTCATTCG	GAG								
SEQ 5	CACTCATTCG	GAG								
SEQ 7	GAACCACAAG	GAC								
SEQ 9 SEQ 11										
SEQ 13	AAATGTTGCG	CAT								
SEQ 15	CAACAACAAG	GAC								
SEQ 17							TCGTGAACAA			
SEQ 18 SEQ 20		CCTCAG								
SEQ 21	AAACTCGGTG	GCC								
SEQ 23	TAATCACAAG	GAT								
SEQ 25										
SEQ 26 SEQ 28										
SEQ 29										
SEQ 32	TATCCATCCT	AAG								
SEQ 34										
SEQ 36 SEQ 37										
SEQ 39										
SEQ 41	GAATCATCCT	CAG								
SEQ 43										
SEQ 82 SEQ 84										
. ,.									1781	1791
	1701	1711	1/21	1/31	1741	1/51	1761			
	####	********	********	********	##					
SEQ 1 SEQ 2							CCTTTTGCCG			
SEQ 2							CCCTTTGCTA			
SEQ 5			CAG	CATATCCACG	CGAAGCCAGG	CTTCCAGGCA	CCCTTTGCTA	TTGCCGTCAA	GAACGCCGTC	GGGGAC
SEQ 7							GACCTGGCCG			
SEQ 9 SEQ 11							CCCTTCGCTG			
SEQ 11							CCCTTGGCTC			
SEQ 15			CAG	AAGATCAACG	TCCACACCTA	CTACCAGATC	GACATGGCCG	AGCAGATCCG	CGCGGCCGTG	CACGAGGCCG
SEQ 17							TTCTTCCTCG			
SEQ 18 SEQ 20							TTCTTCCTCG GACCTGGCAG			
SEQ 21							GACCTGGCAG			
SEQ 23			CAA	AGAATTGAGG	TGAAGGATTG	CTATCAAGTT	CCTTTTGCGG	AAAAGATTAA	GGATCAAGTG	AATGGA
SEQ 25										
SEQ 26 SEQ 28										
SEQ 29										
SEQ 32							GACCTCGCCA			
SEQ 34										
SEQ 36										
SEQ 37 SEQ 39										
SEQ 37 SEQ 39 SEQ 41			CAG	AAAATCAACA	TGTTCAACAC	c				
SEQ 37 SEQ 39 SEQ 41 SEQ 43		GTTTTGCGCA	CAG CCGCAAGGAG	AAAATCAACA TCCAGCCGCA	TGTTCAACAC AGCGGGAGAA	CCTATTTTATC	GAGTTCGCCG	AGGTCATCCG	CAAGGCCGTC	AAGCAC
SEQ 37 SEQ 39 SEQ 41	G	GTTTTGCGCA	CAG CCGCAAGGAG	AAAATCAACA TCCAGCCGCA AAGGTCGCTG	TGTTCAACAC AGCGGGAGAA CTGGTCCCGG	CCTATTTTATC		AGGTCATCCG AGGCGATCAA	CAAGGCCGTC GAAGTCAGTT	AAGCAC GGAGAC

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## 11/17

	1801	1811	1821	1831	1841	1851	1861	1871	1881	1891
SEQ 1	AAGCT	GCTGGTTGCC	GCCGTGGGTG	CCATCACC					AACG	GCAAGCAGGC
SEQ 2	AAGCT	GCTGGTTGCC	GCCGTGGGTG	CCATCACC					AACG	GCAAGCAGGC
SEQ 4	AAACT	CGCAGTGGCA	TCAGTGGGTA	TGATTGCC					AGCG	CGCATTTGGC
SEQ 5	AAACT	CGCAGTGGCA	TCAGTGGGTA	TGATTGCC					AGCG	CGCATTTGGC
SEQ 7			CTTGTGGGTG							
SEQ 9 SEO 11	AAGCT	CCTTGTTGCG	ACGGTGGGCA TGCGTTGGTG	CGATCACG					AACG	ADGATOCTGA
SEQ 11 SEQ 13	CGATG	TTTGATCGCA	TGCAGTGGAG	GATTAGAT					C	GAGACATATT
SEQ 15	GCAAGCAGCT	CCTCGTCGGT	GCCGTCGGCT	TGGTCACC	TCG	GCTGAGATCG	CCAAGGAGAC	CGTCCAGGAG	AAGGAGGATG	GCAGAGTCAC
SEQ 17	TCCCCAAGCT	TCCTCTCATG	GTCACCGGCG	GCTTCCGC					ACTC	GTCAGGGCAT
SEQ 18	TCCCCAAGCT	TCCTCTCATG	GTCACCGGCG	GCTTCCGC					ACTC	GTCAGGGCAT
SEQ 20	AGGTT	GCTCATAGGC	GCGGTCGGCA	ACATCAAC					ACGG	CTGACATTGC
SEQ 21	AGGTT	GCTCATAGGC	GCGGTCGGCA GCTGTCGGAA	ACATCAAC					ACGG	CTCTTACGC
SEQ 23 SEQ 25			GCIGICGGAA							
SEQ 26										
SEQ 28										
SEQ 29										
SEQ 32	AGTGT	ACTTGTTTCA	GCAGTAGGTG	GAATCAAG					A	CTGGACATCT
SEQ 34 SEQ 36										
SEQ 36										
SEQ 39										
SEQ 41										
SEQ 43			ACCGGCGGCT							
SEQ 82	AAGAT	GTTGATCAGC	ACTGTTGGTA AAACGCATGC	GCATCAAG					ATAG	GTACCCTIGC
SEQ 84	ATCGAACC	CGACGCGTCC								GAATGATGGA
	1901		1921	1931	1941	1951	1961	1971	1981	1991
SEQ 1	GAATCAG	ATTCTAG	AGGAGCAG							
SEQ 2	GAATCAG	ATTCTAG	AGGAGCAG							
SEQ 4	CAATTCC	TTGTTGG	AGAAGGAC AGAAGGAC							
SEQ 5	CAATTCC	TTGTTGG	CTGAACCC							
SEQ 7 SEQ 9	GAACAAG	CTGCTTG	AGGAGGAG							
SEQ 11	ATTGCTCAAC	AAATATTTAG	AAGAAGGA							
SEQ 13	TADACTCGAT	CACTUTE ATTG	CTAATGGT							
SEQ 15	CATCCAGCGC	GAGAACGGCG	CCAAGACT							
SEQ 17	GGAGGCC	GCTTTGG	AATCCGAT							
SEQ 18			AATCCGAT AGGGCGCCGA							
SEQ 20 SEQ 21	GCGCGATGTC	GTGGATGAGC	AGGGCGCCGA	GAAGGTGGCC	GAGGCCAAGC	AGACGCATGA	CACCATCGAG	GTCGTGAGCG	AATCACATGG	CGGCAAGACC
SEQ 23	GAATGAAATC	CTAGAAAGTG	GAAAAGCT							
SEQ 25										
SEQ 26										
SEQ 28										
SEQ 29 SEQ 32	TECTEAA	GAGGTTT	TGCAATCT							
SEQ 34										
SEQ 36										
SEQ 37										
SEQ 39										
SEQ 41 SEQ 43			GG							
SEQ 82	GGAGGAG	ATCATCG	CTGGAGGAGA	GGACGATACC						
SEQ 84	AGGTTCC	TACGATT	CGCCCAAC							
	2001	2011	2021	2021	2041	2051	2061	2071	2081	2091
			2021							
SEQ 1 SEQ 2	GATATCGACG	TIGCGCTGGT	TGGCCGTGGG TGGCCGTGGG	TTCCAGAAGG	ATCCCGGTCT	GCCCTCCACC	TTTGCTCAGC	ACCTCGGCGT	C	
SEQ 2 SEO 4	GGACTGGACC	TTGTGCTGGT	TGGACGTGGC	TTCCAGAAGA	ACCCGGGGCT	GGTGTGGGCG	TGGGCCGACG	AGCTGAATGT	A	
SEQ 5	GGACTGGACC	TTGTGCTGGT	TGGACGTGGC	TTCCAGAAGA	ACCCGGGGCT	GGTGTGGGCG	TGGGCCGACG	AGCTGAATGT	A	
SEQ 7	AAGGCGGATG	CCATTCTGAT	AGCCCGTCAG	TTCCTGCGCG	AGCCAGAATG	GGTGTTTTCC	ACGGCGAGAA	AGTTGGGCGT	G	
SEQ 9			GGGACGTGGT							
SEQ 11			CGGTAGAGGA							
SEQ 13 SEQ 15			AGGTAAAGGA TGCCAGGCAG							
SEQ 15 SEQ 17			CGGACGCCCG							
SEQ 18	GATTGCGACA	TGATCGGTAT	CGGACGCCCG	GCCATCATCA	ACCCTTCGCT	TCCCGCCAAC	TTGATCCTCA	ACCCGGAGGT	G	
SEQ 20	AAGGCGGATC	TGGTCCTCAT	TGCTCGCCAG	TTCCTGCGCG	AGCCTGAGTT	TGTGCTGAGG	ACGGCGCATA	ACCTTGGGGT	C	
SEQ 21	AAGGCGGATC	TGGTCCTCAT	TGCTCGCCAG	TTCCTGCGCG	AGCCTGAGTT	TGTGCTGAGG	ACGGCGCATA	ACCTTGGGGT	C	
SEQ 23			CGCAAGGGAG							
SEQ 25 SEQ 26										
SEQ 28										
SEQ 29										
SEQ 32			TGGACGTTGG							
SEQ 34										
SEQ 36 SEQ 37										
SEQ 37										
SEQ 41										
SEQ 43			CGGGCGCGCA							
SEQ 82	CCCTTGGATC	TIGICGCTTC	ACCOUNTAGE	TITITACAACA	ACACTGGACT	I I TO THE STORY	LEGGCTGACG	ATCIGAACAC	T	
SEQ 84			TGGCAAGTTG							

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		2101	2111	2121	2131	2141	2151	2161	2171	2181	2191
							***				
SEQ	1			GAAA	TCTCCATGGC	CAACCAGATC	CGCTGGGGCT	TCACCCGGCG	TGGAGGCACC	CCGTACATTG	ATCCTTCGGT
SEQ							CGCTGGGGCT				
SEQ							CGATGGGGTT				
SEQ				GAGA	TCTCCATGGC	COTTOCAGATO	CGATGGGGTT GGCAGGGCCA	TTTAG	CGGTGCTGGT	CCTTACCTCA	GGAAGAAACI
SEQ SEQ							CGGTGGGGAT				
SEQ				AGAC	TCCACCAGGC	CTTGCAGTTA	GGTTGGGGTT	TCTGGCCCAA	CAAACAACAA	ATTGTTGATT	TGATTGAAAG
SEQ							AAGTTGGCCT				
SEQ							CTCCGTGGTC				
SEQ SEQ							GACAAGAAGA GACAAGAAGA				
SEQ							CACAGAGCAG				
SEQ				AATG	TGCAGTGGCC	TCACCAATAC	CACAGAGCAG	TGTGGCGCAA	GGGTGCAAGG	ATTTGA	
SEQ				AATG	TTGCATGGCC	AGTTCAGTAT	GACTATGCAG	TTAAGGGACA	CAGAAAGTTA	CGTTGA	
SEQ											
SEQ SEQ											
SEO											
SEQ	32			GAGG	TCAAGATGGC	GAACCAGATT	GATTGGAGCT	TCAAGGGACG	TGGAAAGAAA	GTGAACAAGA	GTTCTTTATA
SEQ											
SEQ											
SEQ SEQ											
SEO											
SEQ	43						AGGCTGATGG				
SEQ							GCATGGGGTT				
SEQ	84	TGTCCTACCC	AAGCTGGACC	GAGGATGCTA	GTGTAGCGCT	GATGGGTACC	AGGGCAGCTG	GCAACCCGCA	GTACCATCGC	GTTCACGTGG	CTAAGAAGTG
		2201	2211	2221	2231	2241	2251	2261	2271	2281	2291
	_										
SEQ SEQ		GTACAAGCAG	TCTATTTTCG	ATGTATAG							
SEQ		CGAGAAGATA	TAA	AIGIAIAG							
SEO		CGAGAAGATA	TAA								
SEQ	7										
SEQ		TTATAAGGAG	AGCATCTTTG	AGTAA							
SEQ		AACATCTAAA	TTAGAAGTAA	ATTAG							
SEQ SEQ											
SEQ		GTCCATTGTT	GGTGCTGGTG	TTGAGGTGGT	ACGTCACGTT	CCAACCCCAT	TTGCTTCATT	GTGTTTCCGA	GTATGTCATG	CTGACTTGGT	TCTTTTCTAG
SEQ		GTCCATTGTT	GGTGCTGGTG	TTGAGGTG							
SEQ											
SEQ											
SEQ SEQ											
SEQ											
SEQ	28										
SEQ	28 29										
SEQ SEQ	28 29 32	G									
SEQ SEQ SEQ	28 29 32 34	G									
SEQ SEQ SEQ SEQ	28 29 32 34 36	G									
SEQ SEQ SEQ	28 29 32 34 36 37	G									
SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39	G									
SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43	G					ATCTC	AAACGCCGAC	GAGGTGGCGC	GGGTGACGCA	GTTGATGGCG
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43 82	G						AAACGCCGAC	GAGGTGGCGC	GGGTGACGCA	GTTGATGGCG
SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43 82	G					ATCTC	AAACGCCGAC	GAGGTGGCGC	GGGTGACGCA	GTTGATGGCG
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43 82	G	2311	2321	2331	2341	ATCTC	AAACGCCGAC	GAGGTGGCGC	GGGTGACGCA	GTTGATGGCG
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43 82	G	2311	2321	2331	2341	ATCTC	AAACGCCGAC	GAGGTGGCGC	GGGTGACGCA	GTTGATGGCG
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43 82 84	A	2311 GAGTTGAAGA	2321	2331 TAGACGATCA	2341	ATCTC	AAACGCCGAC 2361 TCTCGTCTCC	GAGGTGGCGC	GGGTGACGCA 2381 CAAGGTATTC	GTTGATGGCG
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43 82 84	G	2311 GAGTTGAAGA	2321 TGATACCTCA	2331 TAGACGATCA	2341 ATGGACCCTT	2351 GCATATTATT GCATATTATT	AAACGCCGAC 2361 TCTCGTCTCC	GAGGTGGCGC 2371 TGCGTATGTT	GGGTGACGCA 2381	GTTGATGGCG 2391 ACAGTAGCTG
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43 82 84	G	2311 GAGTTGAAGA GAGTTGAAGA	2321 TGATACCTCA	2331 TAGACGATCA	2341 ATGGACCCIT	2351 GCATATTATT GCATATTATT	AAACGCCGAC 2361 TCTCGTCTCC	GAGGTGGCGC	GGGTGACGCA 2381 CAAGGTATTC	GTTGATGGCG 2391 ACAGTAGCTG
SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ SEQ	28 29 32 34 36 37 39 41 43 82 84	G	2311 GAGTTGAAGA GAGTTGAAGA	2321 TGATACCTCA	2331 TAGACGATCA	2341 ATGGACCCIT	2351 GCATATTATT GCATATTATT	AAACGCCGAC 2361 TCTCGTCTCC	GAGGTGGCGC	GGGTGACGCA 2381 CAAGGTATTC	GTTGATGGCG 2391 ACAGTAGCTG
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Figure 2. A multiple alignments of the 2031 OR nucleic acid sequence from A. fumigatus (SEQ 1,2) along with related 2031 ORs from other fungi and bacteria (see also Example 4). Regions 1-11, marked with \* or #, refer to regions conserved at the amino acid level between Ors but not OYEs.

Fungal 2031 ORs are given by SEQ ID No.: SEQ ID Nos. 1, 2, 4, 5, and 7, A. fumigatus; SEQ ID No. 9, A.nidulans; SEQ ID Nos. 11 and 13, C. albicans; SEQ ID Nos. 15, 17 and 18, N. crassa; SEQ ID Nos. 20, 21 and 43, M. grisea; SEQ ID No. 23 (NP\_595868), S. pombe; SEQ ID Nos. 25 and 26, C. trifolii; SEQ ID Nos. 28, 29, 31, 32 and 34, F. sporotrichioides; SEQ ID Nos. 36, 37 and 82, F. graminearum; SEQ ID Nos. 39 and 41, M. graminicola; SEQ ID No. 84, U. maydis.

App No.: NYA
Docket No.: HO-P03371US0
Inventor: Sandra E. Lavens et al.
Title: 2031 OXIDOREDUCTASE

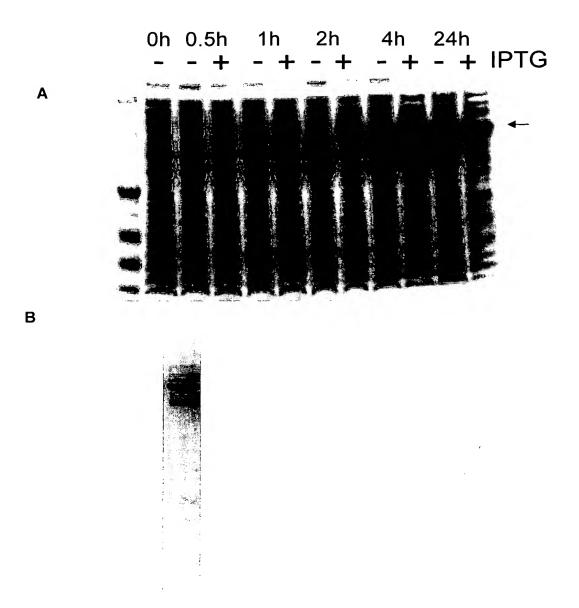


Figure 3. Recombinant 2031 OR. (A) Time course of recombinant 2031 OR induction over 24 hours after the addition of IPTG (samples without IPTG are also shown). The gel was stained with coomassie; A prominent band of the correct molecular weight (marked with an arrow) is seen. (B) Coomassie stained gel showing purified recombinant 2031.

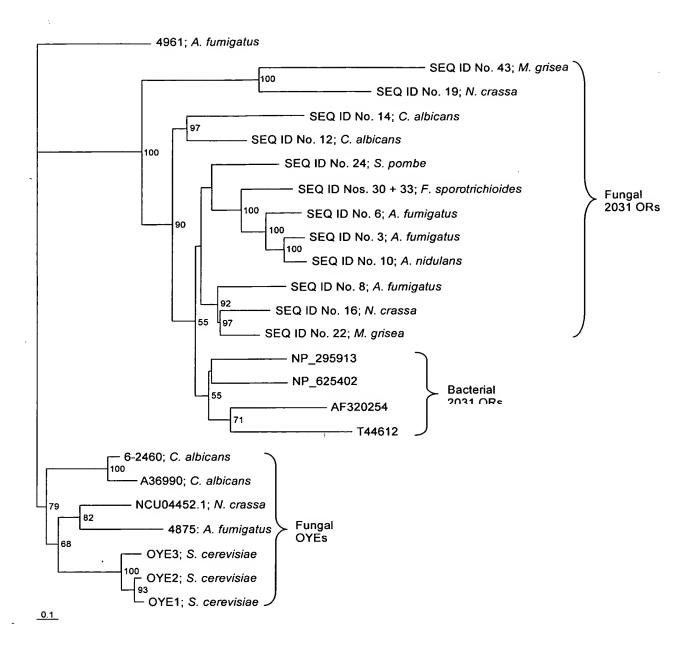


Figure 4. Phylogenetic tree showing relationships between *A. fumigatus* 2031 OR and similar proteins. This demonstrates a 2031 OR clade, which can be distinguished from the OYE proteins.

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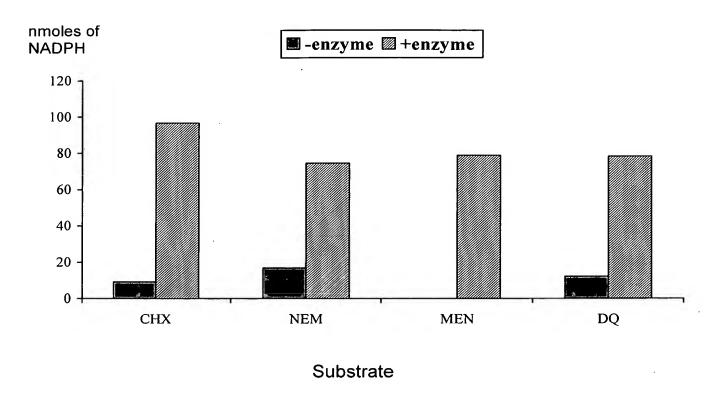


Figure 5: NADPH dehydrogenase activity of recombinant 2031 OR with cyclohexenone (CHX), N-ethylmaleimide (NEM), menadione (MEN) or duroquinone (DQ) as substrates. Final concentrations in the assay were as follows: 500  $\mu$ M substrate, 120  $\mu$ M NADPH, 1  $\mu$ g/200  $\mu$ L 2031 OR.

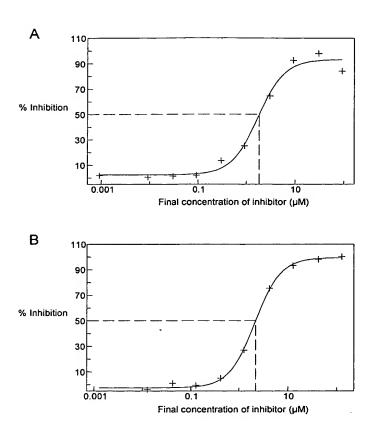


Figure 6: Inhibition of 2031 OR function by two inhibitors (shown in  $\bf A$  and  $\bf B$ ) identified by high-throughput screening.

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